

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 15, 2005, 15:29:19 ; Search time 12873 Seconds
(without alignments)
11352.515 Million cell updates/sec

Title: US-10-751-612-1

Perfect score: 3016

Sequence: 1 tctagacataggcattgta.....gggtatgtcaagtcctatgg 3016

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_hg.*

3: gb_in.*

4: gb_on.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_ey.*

13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	133.2	4.4	279448	8	AY661656
c 2	122.8	4.1	268433	8	AV144442 Sorghum b
3	122.2	4.1	1215	8	U21752 Saccharum h
c 4	118.6	3.9	3688	6	AR412080 Sequence
c 5	118.6	3.9	3688	6	AR473380 Sequence
c 6	118.6	3.9	3688	6	AR488131 Sequence
c 7	118.6	3.9	3691	6	AR412075 Sequence
c 8	118.6	3.9	3691	6	AR473375 Sequence
c 9	118.6	3.9	3691	6	AR488126 Sequence
c 10	118.6	3.9	5174	6	AR412079 Sequence
c 11	118.6	3.9	5174	6	AR473379 Sequence
c 12	118.6	3.9	5174	6	AR488130 Sequence
c 13	118.6	3.9	5174	8	AF093505 Saccharum b
c 14	106.4	3.5	183990	8	AF114171 Sorghum b
c 15	74.8	2.5	183990	8	AF114171 Sorghum b
c 16	73.8	2.4	157237	8	AY542311 Sorghum b
c 17	72.4	2.4	147461	8	AP004691 Oryza sat
c 18	72.4	2.4	148544	8	AP004636 Oryza sat
c 19	70.2	2.3	202197	8	AF466200 Sorghum b

c 20	69.8	2.3	136068	8	AC137693	AC137693 Oryza sat
c 21	68.4	2.3	3039	8	ZMU34726	U34726 Zea mays su
c 22	67	2.2	4636	8	AV177889	AV177889 Sorghum b
c 23	67	2.2	138858	8	AP002968	AP002968 Oryza sat
c 24	67	2.2	142376	8	AF503433	AF503433 Sorghum b
c 25	67	2.2	202197	8	AF466200	AF466200 Sorghum b
c 26	66.8	2.2	165745	8	OSJN00105	OSJN00105 Sorghum b
c 27	66.2	2.2	144159	8	AF466199	AF466199 Sorghum b
c 28	65.4	2.2	1334	6	AX406684	AX406684 Sequence
c 29	65.4	2.2	120132	8	AC120496	AC120496 Genomic s
c 30	65.4	2.2	129802	8	AP005447	AP005447 Oryza sat
c 31	65.4	2.2	162249	8	AF061282	AF061282 Sorghum b
c 32	64.8	2.1	121894	8	AC135599	AC135599 Oryza sat
c 33	64.4	2.1	144159	8	AF466199	AF466199 Sorghum b
c 34	64.4	2.1	150286	2	OSJN00241	OSJN00241 Sorghum b
c 35	63.8	2.1	135991	8	AP002882	AP002882 Oryza sat
c 36	63.8	2.1	162249	8	AF061282	AF061282 Sorghum b
c 37	63.8	2.1	182779	8	AP002845	AP002845 Oryza sat
c 38	63.4	2.1	165909	8	AP005420	AP005420 Oryza sat
c 39	63.4	2.1	187410	8	AP005579	AP005579 Oryza sat
c 40	62.8	2.1	103167	8	AY661658	AY661658 Sorghum b
c 41	62.8	2.1	125927	8	AY661657	AY661657 Sorghum b
c 42	62.6	2.1	795	11	AF344051	AF344051 Oryza sat
c 43	62.4	2.1	113332	8	CNS08C72	AL731750 Oryza sat
c 44	62.4	2.1	151117	8	CNS08C96	AL732531 Oryza sat
c 45	61.8	2.0	148736	8	OSJN00134	AL662944 Oryza sat

ALIGNMENTS

RESULT 1
AY661656
LOCUS AY661656 279448 bp DNA linear PLN 03-JUL-2004
DEFINITION Sorghum bicolor clone BAC 88M4, complete sequence.
ACCESSION AY661656
VERSION AY661656.1 GI:49359135
KEYWORDS HTG.
SOURCE Sorghum bicolor (sorghum)
ORGANISM Sorghum bicolor

REFERENCE 1 (bases 1 to 279448)
AUTHORS Islam-Faridi, M.N., Kim, J.-S., Klein, P.E., Stelly, D.M., Price, H.J., Klein, R.R. and Mullet, J.E.
TITLE Cytogenetic Analysis of Sorghum Chromosome 3 and Alignment to Rice Chromosome 1 Reveals Expansion of Pericentromeric Heterochromatin in Sorghum

JOURNAL Unpublished (2004)
REFERENCE 2 (bases 1 to 279448)
AUTHORS Klein, R.R., Klein, P.E., Mullet, J.E., Minx, P. and Miner, T.L.
TITLE Direct Submission
JOURNAL Submitted (21-JUN-2004) USDA-ARS, Southern Plains Agricultural Research Center, 2765 F&B Road, College Station, TX 77845, USA

FEATURES
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1. 279448
Location/Qualifiers
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ORIGIN

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Best Local Similarity 77.1%; Pred. No. 2.2e-23;
Matches 162; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

Qy 1457 CTAAGGCCAGTCTCAGTGGGTTTCATCAGATTTTCATGACATTAATAAGCTGATGCTG 1516
Db 131606 CTAAGGTCAGTCTCAATGATGATTTTTCAGAGTTTATGGGCATTAAATGCTGATGCTA 131665

QY 1517 ACACCGTATTGATGAAGAGAGAGATGATAAGAGTTTTCATGCGAGTAGAGAGAGTTTCATG 1576
 Db 131666 ACATCGTATTATAAGTGAGAGATGATAAGAGTTTTCATGGGAGCAGAGAGTTTCATC 131725
 QY 1577 GGGATGAACCTCTTCTCACTGTTTCCAAAATATAGATGCATTGTTGAAGAGGGCCATGAA 1636
 Db 131726 CCCATAAACTCTTCTGCACGTCTTCTAAATCAGATGTGTGAAACTGGGACACGAA 131785
 QY 1637 ATCTTAGTACACTGACCTAGATGAGAT 1666
 Db 131786 CTCTCCATTGACACTGACCTAGCAGAGTT 131815

RESULT 2
 AY144442/c 268433 bp DNA linear PLN 08-JAN-2003
 LOCUS Sorghum bicolor BAC 95A23/98N8.1 Rph region, partial sequence.
 DEFINITION
 ACCESSION AY144442
 VERSION AY144442.1 GI:27542750
 KEYWORDS
 SOURCE Sorghum bicolor (sorghum)
 ORGANISM
 Sorghum bicolor
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Sorghum.
 REFERENCE
 AUTHORS 1 (bases 1 to 268433)
 Ramakrishna, W., Emberton, J., SanMiguel, P., Ogden, M., Llaca, V.,
 Messing, J. and Bennetzen, J.L.
 TITLE Comparative sequence analysis of the sorghum rph region and the
 maize rpl resistance gene complex
 JOURNAL Plant Physiol. 130 (4), 1728-1738 (2002)
 MEDLINE 22369073
 PUBMED 12481055
 REFERENCE 2 (bases 1 to 268433)
 Ramakrishna, W., Emberton, J., SanMiguel, P., Ogden, M., Llaca, V.,
 Linton, E., Messing, J. and Bennetzen, J.L.
 TITLE Sequence and physical map analysis of Rpl region of maize and
 sorghum
 JOURNAL Unpublished
 REFERENCE 3 (bases 1 to 268433)
 Ramakrishna, W., Emberton, J., SanMiguel, P., Ogden, M., Llaca, V.,
 Linton, E., Messing, J. and Bennetzen, J.L.
 TITLE Direct Submission
 JOURNAL Submitted (26-AUG-2002) Biological Sciences, Purdue University,
 Hansen Bldg, West Lafayette, IN 47907, USA
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Query Match 4.1%; Score 122.8; DB 8; Length 268433;
Best Local Similarity 74.8%; Pred. No. 1.2e-20;

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Matches 154; Conservative 0; Mismatches 52; Indels 0; Gaps 0;
Qy 1453 GTTCTTAAGGCCACTCTCAGTGGGTTTCATCAGAGTTTCATGACATTAATAAGCTGA 1512
Db 238542 GCTTCTTAGGCCAGTCTCAATGAGGGTTTCATTAGAGTTTCATGACATTAATAAGCTGA 238483
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Db 238482 TGTGGCACTATATTAAATGAAGAGAGAGATGTTAAGAGTTTCATGGAGTAGAGAGTTT 238423
Qy 1573 CATGGGATGAACCTCTTCTTCACTGTTTCCAAAATATAGATGATGTTGTAAGAGGGCA 1632
Db 238422 CATCCCATAAACTCTCTATGCACTGTTTCCAAAATATGATGTTGTAAGAACTGTGTCA 238363
Qy 1633 TGAATCTCTAGTCACACTGACCTAA 1658
Db 238362 TGAACCTTCATTAAAGATGCCCTTA 238337

RESULT 3
SCFGLUTRAA 1215 bp mRNA linear PLN 02-APR-1999
LOCUS Saccharum hybrid cultivar H65-7052 glucose transporter mRNA,
DEFINITION partial cds.
ACCESSION L21752
VERSION L21752.1 GI:347852
KEYWORDS Saccharum hybrid cultivar H65-7052
SOURCE Saccharum hybrid cultivar H65-7052
ORGANISM Saccharum hybrid cultivar H65-7052
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
complex.
REFERENCE 1 (bases 1 to 1215)
AUTHORS Bugos,R.C. and Thom,M.
TITLE Glucose transporter cDNAs from sugarcane
JOURNAL Plant Physiol. 103 (4), 1469-1470 (1993)
MEDLINE 94120022
PUBMED 8290645
REFERENCE 2 (bases 1 to 1215)
AUTHORS Bugos,R.C.
TITLE Direct Submission
JOURNAL Submitted (14-JUL-1993) Robert Bugos, Hawaiian Sugar Planters'
Association, Experiment Station, Aiea, HI 96701-1057, USA
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CDS
3'UTR
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Query Match 4.1%; Score 122.2; DB 8; Length 1215;
Best Local Similarity 82.4%; Pred. No. 1.1e-20;
Matches 164; Conservative 0; Mismatches 33; Indels 2; Gaps 2;

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QY 1522 GTATTGATGAAGAGAGAGATGATAGAGTTTCATCGAGTAGAGAGTTTCATGG-GGA 1580
Db 1028 GTATTGAATGAAGTAGAGATGATAGAGTTTCATCGGAGTAGAGAGTTTATGGAGGA 1087
QY 1581 TGAAGTCTCTTCTCACTGTTTCCAAATATAGATGATTCATGGTAAGAGGGCCATGAATCT 1640
Db 1088 TGAAGTCTCTTCTCACTGTTTCCAAATATAGATGATTCATGGTAAGAGGGCCATGAATCT 1146
QY 1641 CTAGTGACACTGACCTTAAG 1659
Db 1147 ATTGAGACTGGTATGTAAG 1165

RESULT 4
AR412080/c AR412080 3688 bp DNA linear PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 10 from patent US 6638766.
ACCESSION AR412080
VERSION AR412080.1 GI:40164633
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 3688)
AUTHORS Albert,H.H. and Wei,H.
TITLE Promoter of the sugarcane UB14 gene
JOURNAL Patent: US 6638766-A 10 28-OCT-2003;
FEATURES Location/Qualifiers
source 1..3688
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ORIGIN
Query Match 3.9%; Score 118.6; DB 6; Length 3688;
Best Local Similarity 86.0%; Pred. No. 1.1e-19;
Matches 166; Conservative 0; Mismatches 24; Indels 3; Gaps 3;

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Db 1914 AGTTTCTGAGGCCGCTCTCAGT-GGATTTTCATCAGAGTTTCATGACATTAATAAGCT 1856
QY 1511 GATGTGACACCGTATTGATGAAGAGAGATGATAGAGTTTCATCGAGTAGAGAGCT 1570
Db 1855 GATGTGACACCGTATTGATGAAGAGAGATGATAGAGTTTCATCGAATTAGAGAGCT 1796
QY 1571 TTCAATGGGATGAAGTCTTT-CTTCACTGTTTCCAAATAT-AGATGCAATTGGTAAGAGG 1628
Db 1795 TTACGAAGATGAAGTCTTCTCTGCACTGTTTCCAAATATGGGTTGCATTAATAACATG 1736
QY 1629 GCCATGAATCTC 1641
Db 1735 GCCATAAAATCCC 1723

RESULT 5
AR473380/c AR473380 3688 bp DNA linear PAT 20-FEB-2004
LOCUS
DEFINITION Sequence 10 from patent US 6686513.
ACCESSION AR473380
VERSION AR473380.1 GI:42708831
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 3688)
AUTHORS Albert,H.H. and Wei,H.
TITLE Sugarcane ubi9 gene promoter sequence and methods of use thereof
JOURNAL Patent: US 6686513-A 10 03-FEB-2004;
FEATURES Location/Qualifiers
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Best Local Similarity 86.0%; Pred. No. 1.1e-19;
Matches 166; Conservative 0; Mismatches 24; Indels 3; Gaps 3;

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Db 1795 TTACGAAGATGAAGTCTTCTCTGCACTGTTTCCAAATATGGGTTGCATTAATAACATG 1736
QY 1629 GCCATGAATCTC 1641
Db 1735 GCCATAAAATCCC 1723

RESULT 7
AR412075/c AR412075 3691 bp DNA linear PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 3 from patent US 6638766.
ACCESSION AR412075
VERSION AR412075.1 GI:40164628
FEATURES Location/Qualifiers
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QY 1629 GCCATGAATCTC 1641
Db 1735 GCCATAAAATCCC 1723

RESULT 7
AR412075/c AR412075 3691 bp DNA linear PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 3 from patent US 6638766.
ACCESSION AR412075
VERSION AR412075.1 GI:40164628
FEATURES Location/Qualifiers
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KEYWORDS SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 3691)
AUTHORS Albert,H.H. and Wei,H.
TITLE Promoter of the sugarcane UB14 gene
JOURNAL Patent: US 6638766-A 3 28-OCT-2003;
FEATURES Location/Qualifiers
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Db 1855 GATGTGGCACCCTATTGATGAAGAGAGAGATGAAGAGTTTCATGGAATTAGAGAGAGT 1796
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QY 1629 GCCATGAATCTC 1641
Db 1735 GCCATAAAATCCC 1723
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LOCUS AR473375 3691 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 3 from patent US 6686513.
ACCESSION AR473375
VERSION AR473375.1 GI:42708826
KEYWORDS SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 3691)
AUTHORS Albert,H.H. and Wei,H.
TITLE Sugarcane ubi9 gene promoter sequence and methods of use thereof
JOURNAL Patent: US 6686513-A 3 03-FEB-2004;
FEATURES Location/Qualifiers
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QY 1629 GCCATGAATCTC 1641
Db 1735 GCCATAAAATCCC 1723
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LOCUS AR488126 3691 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 3 from patent US 6706948.
ACCESSION AR488126
VERSION AR488126.1 GI:47253891
KEYWORDS SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 3691)
AUTHORS Albert,H.H. and Wei,H.
TITLE Sugarcane UB19 gene promoter and methods of use thereof
JOURNAL Patent: US 6706948-A 3 16-MAR-2004;
FEATURES Location/Qualifiers
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QY 1629 GCCATGAATCTC 1641
Db 1735 GCCATAAAATCCC 1723
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LOCUS AR412079 5174 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 8 from patent US 6638766.
ACCESSION AR412079
VERSION AR412079.1 GI:40164632
KEYWORDS SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 5174)
AUTHORS Albert,H.H. and Wei,H.
TITLE Promoter of the sugarcane UB14 gene
JOURNAL Patent: US 6638766-A 8 28-OCT-2003;
FEATURES Location/Qualifiers
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QY 1629 GCCATGAATCTC 1641
Db 1735 GCCATAAATCCC 1723

RESULT 14
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LOCUS Sorghum bicolor BAC clone 25.M18, complete sequence.
DEFINITION AF114171
ACCESSION AF114171
VERSION AF114171.1 GI:4680196
KEYWORDS Sorghum bicolor (sorghum)
SOURCE Sorghum bicolor
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE 1 (bases 1 to 183990)
AUTHORS Llaca,V., Lou,A., Young,S. and Messing,J.
TITLE Retrotransposable elements of Sorghum bicolor
JOURNAL unpublished
REFERENCE 2 (bases 1 to 183990)
AUTHORS Llaca,V., Lou,A., Young,S. and Messing,J.
TITLE Direct Submision
JOURNAL Submitted (15-DEC-1998) Waksman Institute, Rutgers University, 190
Frelinghuysen Rd., Piscataway, NJ 08854-8020, USA
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1619 TGGTAA 1624
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AF114171/c 183990 bp DNA linear PLN 25-APR-1999
LOCUS Sorghum bicolor BAC clone 25.M18, complete sequence.
DEFINITION AF114171
ACCESSION AF114171
VERSION AF114171.1 GI:4680196
KEYWORDS
SOURCE Sorghum bicolor (sorghum)
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
AUTHORS 1 (bases 1 to 183990)
Llaca,V., Lou,A., Young,S. and Messing,J.
TITLE Retrotransposable elements of Sorghum bicolor
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 183990)
Llaca,V., Lou,A., Young,S. and Messing,J.
AUTHORS Direct Submission
TITLE Submitted (15-DEC-1998) Waksman Institute, Rutgers University, 190
Frelinghuysen Rd., Piscataway, NJ 08854-8020, USA
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Wed Feb 16 17:07:28 2005

us-10-751-612-1.l.rge

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/translation="MSGGIQDDSLIWLIVRMIPRYKQVLSFLGWSHGIRCOHPSID
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LSLDLNISETFAFVASLLHPESAALATARSCLAAASGSAQASSTLKRWFSW
IDRATSFITTTVTIERTLGMIEHCKDQVQDEIRSLRPQDFARVAVNFKIDEYPSR
DNAVLSDPNICTNIESPVLQIAPRPPPLSPVCSRNLCRPGAHVACALCVWRG
RCRCRRWNTTGRQMLIFMPADYYTHVTIIVDDDDSIHALLLVLLACGQLLALC
TIVVHLRCT"
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/rpt_family="HCSR-4"
/rpt_type=dispersed
/mRNA complement(join(<46323..46753,47300..47458,48167..48248))
/product="hypothetical protein"
/CDS complement(join(46323..46753,47300..47458,48167..48248))
/note="similar to Oryza sativa EST clone C3025_1A"
/codon_start=1
/product="hypothetical protein"
/protein_id="AAD27561.1"
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Query Match 2.5%; Score 74.8; DB 8; Length 183990;
Best Local Similarity 63.2%; Pred. No. 5.8e-08;
Matches 115; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 2450 ATAAAGAGTTAAATGCATGGTAGGCTCTTGATCTTGTCTGAGAGTGCCACTTAGTCCAC 2509
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
82480 ATAAAGAGTAAATTGCAGGCGCGTCTTAAAGTATTATGTGTTTTCATCTAGGTCCTC 82421

QY 2510 AACTCTCAATTCGATTTTTCACACCCCTAATGTTATTCAGTGTGCCACTTAGATCTAC 2569
Db || || || || || || || || || || || || || || || || || || || || ||
82420 AAGCTATGAATGCATGCTGACTCTCTAATGTTATTTAAGTGATCTATCTAGGTCCTC 82361

QY 2570 AACTCTCAAAATGCATTTCTGATACCCCTAGTGTGTTTCAAGTGTGTCTAGTGAAGA 2629
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
82360 AACTAGAAATGCACGCTGACTCTCTAATGTTATTTAAGTGATCTCATCTAGGTCCTCA 82301

QY 2630 AA 2631
Db ||
82300 AA 82299
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Search completed: February 16, 2005, 07:44:40
Job time : 12881 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 15, 2005, 14:41:05 ; Search time 1550 Seconds
(without alignments)
11518.671 Million cell updates/sec

Title: US-10-751-612-1

Perfect score: 3016

Sequence: 1 tctagagcataggcatgtta.....gggctagtccaagtcctatgg 3016

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
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- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3016	100.0	3016	13 ADR21935	ADR21935 Sugarcane
C 2	118.6	3.9	3688	2 AAZ28438	Aaz28438 Sugar can
C 3	118.6	3.9	3688	12 ADK66212	Adk66212 Sugarcane
C 4	118.6	3.9	3691	2 AAZ28433	Aaz28433 Ub19 gene
C 5	118.6	3.9	3691	12 ADK66205	Adk66205 Sugarcane
C 6	118.6	3.9	5174	2 AAZ28437	Aaz28437 Sugar can
C 7	118.6	3.9	5174	12 ADK66210	Adk66210 Sugarcane
C 8	65.8	2.2	2000	12 ADJ40707	Adj40707 Plant cDN
C 9	65.4	2.2	1334	6 ABK93956	Abk93956 cDNA enco
C 10	62	2.1	701	12 ADJ48000	Adj48000 Maize oil
C 11	61.2	2.0	290	7 ADS68705	Ads68705 Corn seed
C 12	60.4	2.0	2000	8 ADA72001	Ada72001 Rice gene
C 13	59	2.0	2010	10 ADC08563	Adc08563 Rice DNA
C 14	57.6	1.9	2000	12 ADJ41371	Adj41371 Plant cDN
C 15	53.4	1.8	2010	10 ADC08563	Adc08563 Rice DNA
C 16	53	1.8	5955	12 ADH22268	Adh22268 Rice PONG
C 17	52.6	1.7	1710	3 AAZ299113	Aaz299113 Phosphoen
C 18	52.6	1.7	1973	3 AAZ299112	Aaz299112 Phosphoen
C 19	52.6	1.7	2000	12 ADJ41371	Adj41371 Plant cDN
C 20	52.4	1.7	2000	8 ADA72420	Ada72420 Rice gene

C 21	52.4	1.7	2000	12 ADJ41383	Adj41383 Plant cDN
C 22	51.8	1.7	5955	12 ADH22268	Adh22268 Rice PONG
C 23	51.6	1.7	1150	8 ADA73250	Ada73250 Rice gene
C 24	51.6	1.7	2000	8 ADA71938	Ada71938 Rice gene
C 25	51.6	1.7	2000	8 ADA73161	Ada73161 Rice gene
C 26	51.4	1.7	2000	8 ADA71483	Ada71483 Rice gene
C 27	51.2	1.7	2000	8 ADA71894	Ada71894 Rice gene
C 28	51.2	1.7	2000	8 ADA71798	Ada71798 Rice gene
C 29	51.2	1.7	2000	8 ADA73446	Ada73446 Rice gene
C 30	50.2	1.7	76363	8 ACF30938	Acf30938 Rice cult
C 31	50.2	1.7	76363	12 ADI09997	Adi09997 Rice cult
C 32	50.2	1.7	76363	12 ADK72433	Adk72433 Rice fert
C 33	50	1.7	1334	6 ABK93956	Abk93956 cDNA enco
C 34	50	1.7	2000	12 ADJ41455	Adj41455 Plant cDN
C 35	50	1.7	76363	8 ACF30938	Acf30938 Rice cult
C 36	50	1.7	76363	12 ADI09997	Adi09997 Rice cult
C 37	50	1.7	76363	12 ADK72433	Adk72433 Rice fert
C 38	49.4	1.6	2000	8 ADA71938	Ada71938 Rice gene
C 39	48.8	1.6	2000	8 ADA72001	Ada72001 Rice gene
C 40	48.8	1.6	2000	12 ADJ40785	Adj40785 Plant cDN
C 41	48.2	1.6	2000	12 ADJ40688	Adj40688 Plant cDN
C 42	47.4	1.6	2000	8 ADA72420	Ada72420 Rice gene
C 43	47.4	1.6	2000	12 ADJ41383	Adj41383 Plant cDN
C 44	46	1.5	260	12 ADQ04630	Adq04630 Maize hom
C 45	45.8	1.5	2000	8 ADA72815	Ada72815 Rice gene

ALIGNMENTS

RESULT 1

ADR21935
ID ADR21935 standard; DNA; 3016 BP.

XX AC ADR21935;

XX DT 21-OCT-2004 (first entry)

XX DE Sugarcane O-methyl transferase (OMT) promoter DNA SeqID 1.

XX KW O-methyl transferase; OMT; promoter; stem-specific; defence-inducible;
carbon metabolism; insecticidal; pest tolerance; plant; ds.

XX OS Saccharum.

XX FH Key Location/Qualifiers

FT CAAT_signal 2661..2664

FT TATA_signal 2849..2855

FT misc_feature 3013..3015

FT /note= "Start codon (AUG) of OMT"

FT /tag= a

FT /tag= b

FT /tag= c

FT /note= "Start codon (AUG) of OMT"

XX WO2004062365-A2.

XX PD 29-JUL-2004.

XX PP 05-JAN-2004; 2004WO-US000113.

XX PR 03-JAN-2003; 2003US-0437890P.

XX PA (TEXA) UNIV TEXAS A & M SYSTEM.

XX PI Mirkov TE, Dama MB, Reddy AS, Thomas TL, Rathore KS, Emani C;

XX PI Kumpatla SP;

XX DR WPI; 2004-544018/52.

XX XX New isolated nucleic acid comprises an o-methyl transferase (OMT)

PT promoter and an exogenous nucleic acid, useful as a promoter for altering

PT carbon metabolism in a plant cell or for driving expression of

PT insecticidal proteins in sugarcane.

Db 1801 TAAGTAAATGCTTTGGCTTCATCACCGGCTTAATGCTCGACAGAAAAACACGTCGGT 1860
Qy 1861 AGTCAAGGTTGGCTTAACAACTGGGTTACATGTAAACACGTTTCATGCTTAGAAA 1920
Db 1861 AGTCAAGGTTGGCTTAACAACTGGGTTACATGTAAACACGTTTCATGCTTAGAAA 1920
Qy 1921 CGGCTCGAGGATTTAGATACAACTTTCAATTTATATCTTTAGGGCCCTCCAAATATTGTGAG 1980
Db 1921 CGGCTCGAGGATTTAGATACAACTTTCAATTTATATCTTTAGGGCCCTCCAAATATTGTGAG 1980
Qy 1981 CTCTAAACTAGTTTATGTCACGGTGGAGAGGAGGCTTAAATAATAATCTTTGAG 2040
Db 1981 CTCTAAACTAGTTTATGTCACGGTGGAGAGGAGGCTTAAATAATAATCTTTGAG 2040
Qy 2041 CTAAGCTGAAGAGAGCTATTTTTTTTCTGCTCCCAATACATGATAGATACATATGA 2100
Db 2041 CTAAGCTGAAGAGAGCTATTTTTTTTCTGCTCCCAATACATGATAGATACATATGA 2100
Qy 2101 GAGAAAAATATATGAATAAAGAACACTTTATCATGCCAGCCATACAAATAGAGATTTTCAT 2160
Db 2101 GAGAAAAATATATGAATAAAGAACACTTTATCATGCCAGCCATACAAATAGAGATTTTCAT 2160
Qy 2161 CTAAGAGCAAACACCTGACTCGTACTGTGTAAGGTGCTCTAGTTGGAGTGGTGCATCTTT 2220
Db 2161 CTAAGAGCAAACACCTGACTCGTACTGTGTAAGGTGCTCTAGTTGGAGTGGTGCATCTTT 2220
Qy 2221 TAGTTGTTAGTAGTGAAGCTAGTTTAGTGCTCTTTTCTGCTAGGTTTATGTTGTG 2280
Db 2221 TAGTTGTTAGTAGTGAAGCTAGTTTAGTGCTCTTTTCTGCTAGGTTTATGTTGTG 2280
Qy 2281 TTTTGGCTGCCAAGTGTGTAACAACTCAAGGTAAAGTCCCATCTAATCTTAAATATGATGC 2340
Db 2281 TTTTGGCTGCCAAGTGTGTAACAACTCAAGGTAAAGTCCCATCTAATCTTAAATATGATGC 2340
Qy 2341 CAAATAAAGATAGATTACAAAGTTTAAACGACGGAAGAACTCTAAATAGGATGGAAGTT 2400
Db 2341 CAAATAAAGATAGATTACAAAGTTTAAACGACGGAAGAACTCTAAATAGGATGGAAGTT 2400
Qy 2401 TTGTAGATTAATTAATGTTATGATGAGTGGAGTGCACCAACCAACATTAAGAGTTA 2460
Db 2401 TTGTAGATTAATTAATGTTATGATGAGTGGAGTGCACCAACCAACATTAAGAGTTA 2460
Qy 2461 AATGATGATGAGTCTTGTATCTCTGAGGTTGCCACTTAGGTCCACAACTCTCAA 2520
Db 2461 AATGATGATGAGTCTTGTATCTCTGAGGTTGCCACTTAGGTCCACAACTCTCAA 2520
Qy 2521 TTGCATTTTTCACACCCCTTAATGTTATCAAGTGTGCCACTTAGATCTACAACTCTCAA 2580
Db 2521 TTGCATTTTTCACACCCCTTAATGTTATCAAGTGTGCCACTTAGATCTACAACTCTCAA 2580
Qy 2581 ATGCATTTTTCATACCCCTAGTGTGTTCAAGTGTGCTACTTAGGCAAGAAAGTTAGTA 2640
Db 2581 ATGCATTTTTCATACCCCTAGTGTGTTCAAGTGTGCTACTTAGGCAAGAAAGTTAGTA 2640
Qy 2641 ATTTTATAAGCTATGGACCAAAATAATTTATGATGATGCTCGAAGTCTAGTATGATAT 2700
Db 2641 ATTTTATAAGCTATGGACCAAAATAATTTATGATGATGCTCGAAGTCTAGTATGATAT 2700
Qy 2701 GATGACCCCAATAATAGACACTAGTTCATGCGCTGGTTTCTTGTATAGTACTAGTATG 2760
Db 2701 GATGACCCCAATAATAGACACTAGTTCATGCGCTGGTTTCTTGTATAGTACTAGTATG 2760
Qy 2761 ATAACCTTTTCAAGTGTAGTACTACTTATAGTCTTATAGTCCGATATACAAATATA 2820
Db 2761 ATAACCTTTTCAAGTGTAGTACTACTTATAGTCTTATAGTCCGATATATACAAATATA 2820
Qy 2821 GAATTCGGAAGTACTATAAACGGAGGCTTATAAATGGAGAGCTTTTGCATCATGAGGCTA 2880
Db 2821 GAATTCGGAAGTACTATAAACGGAGGCTTATAAATGGAGAGCTTTTGCATCATGAGGCTA 2880
Qy 2881 TAACAACTTTGAGCAAAAAACAGAACCGGCTCGCGCATGGGCTCAGCAAGGAGCAACACACA 2940

Db 2881 TAACAACTTTGAGCAAAAAACAGAACCGGCTCGCGCATGGGCTCAGCAAGGAGCAACACACA 2940
Qy 2941 AGCACTGATCAGCAGGCGCTGCTGGATGCTCAGTCCAGCTCTGGCACCACACCTGGGC 3000
Db 2941 AGCACTGATCAGCAGGCGCTGCTGGATGCTCAGTCCAGCTCTGGCACCACACCTGGGC 3000
Qy 3001 TATGTCGAAGTCCATGG 3016
Db 3001 TATGTCGAAGTCCATGG 3016
RESULT 2
AAZ28438/C
ID AAZ28438 standard; DNA; 3688 BP.
XX
AC AAZ28438;
XX
DT 23-DEC-1999 (first entry)
XX
DE Sugar cane ubi9 gene fragment used in the construction of pubi9-GUS.
XX
KW Ubiquitin gene; ubi9; promoter; initiation codon; intron; monocotyledon;
KW dicotyledon; disease resistance; environmental stress; sugar cane;
KW pubi4-GUS; reporter plasmid; beta-glucuronidase; GUS; ss.
XX
OS Saccharum sp.
XX
PN WO9946976-A1.
XX
PD 23-SEP-1999.
XX
PF 18-MAR-1999; 99WO-US005985.
XX
PR 19-MAR-1998; 98US-0078768P.
PR 17-MAR-1999; 99US-00270976.
XX
PA (UYHA-) UNIV HAWAII.
PA (USDA) US DEPT OF AGRICULTURE.
XX
PI Albert HH, Wei H;
XX
DR WPI; 1999-590952/50.
XX
PT New nucleotide sequences derived from sugarcane polyubiquitin genes
PT useful in regulating expression of nucleic acid sequences in
PT monocotyledonous and dicotyledonous plants.
XX
PS Claim 11; Fig 11; 118pp; English.
XX
CC This sequence corresponds to nucleotides 1-3688 of the sugar cane
CC ubiquitin 9 (ubi9) gene AAZ28437. This fragment of the gene was ligated
CC to the gene encoding beta glucuronidase (GUS) in the generation of the
CC reporter plasmid pubi9-GUS and 9PI-GUS. The plasmids are used in the
CC methods of the invention, which relates to nucleotide sequences derived
CC from sugar cane polyubiquitin genes. Ubi4 and ubi9 genes are used in the
CC invention as they have linked promoter activity. The genes can be used to
CC regulate the expression of nucleic acid sequences introduced in to
CC dicotyledonous and monocotyledonous plants. The nucleic acid sequences
CC (ubi4 and ubi9) are used to create plants with commercially useful
CC phenotypes. High levels of protein expression aid the generation of
CC plants which exhibit commercially important phenotypic properties such as
CC pest and disease resistance, resistance to environmental stress and
CC improved qualities
XX
SQ Sequence 3688 BP; 844 A; 862 C; 925 G; 1055 T; 0 U; 2 Other;
Query Match 3.9%; Score 118.6; DB 2; Length 3688;
Best Local Similarity 86.0%; Pred. No. 5.4e-22;
Matches 166; Conservative 0; Mismatches 24; Indels 3; Gaps 3;
Qy 1451 AGTTTCTTAAGCCAGTCTCAGTGGGTTTCATCAGAGTTTCATGAGCAATTAAATAGCT 1510
Db 1914 AGTTTCTTAAGCCCGTCTCAGT-GGATTTTCATCAGAGTTTCATGAGCAATTAAATAGCT 1856

QY 1511 GATGTGACACCGTATTGATGAAGAGAGAGATGATAAGAGTTTCATGCGAGTAGAGAGAGT 1570
 |||||
 Db 1855 GATGTGGCACCGTATTGATGAAGAGAGAGATGATAAGAGTTTCATGCGAATTAGAGAGAGT 1796
 |||||
 QY 1571 TTTCATGGGATGAACACTCTT-CTTCACCTGTTTCCAAAATAT-AGATGCAATTGGTAAGAGG 1628
 |||||
 Db 1795 TTTCAGGAAGATGAACACTCTTCTCGCACTGTTTCCAAAATATGGTTGCATTAAATACATG 1736
 |||||
 QY 1629 GCCATGAATCTC 1641
 |||||
 Db 1735 GCCATAAAATCCC 1723
 |||||
 RESULT 3
 ADR66212/c
 ID ADR66212 standard; DNA; 3688 BP.
 XX AC ADR66212;
 XX 06-MAY-2004 (first entry)
 XX Sugarcane polyubiquitin ubi9 gene promoter DNA.
 DE XX
 XX Polyubiquitin; monocotyledonous; dicotyledonous; transgenic plant;
 KW phenotypic; sugarcane; plant; ds.
 XX OS
 XX Saccharum sp.
 XX FH Key Location/Qualifiers
 FT misc_feature 1
 FT /*tag= a
 FT /note= "Upstream of 5' UTR"
 FT 2249..2313
 FT /*tag= b
 FT 2314..3688
 FT intron
 FT /*tag= c
 FT US6686513-B1.
 XX PN
 XX 03-FEB-2004.
 XX PD
 XX 20-OCT-2000; 2000US-00693467.
 XX PF
 XX 19-MAR-1998; 98US-0078767P.
 XX PR 17-MAR-1999; 99US-00270976.
 XX PA (USDA) US SEC OF AGRIC.
 XX (UYHA-) UNIV HAWAII.
 XX PI Albert HH, Wei H;
 XX WPI; 2004-106365/11.
 XX DR
 XX New transgenic plant cell comprising the sugarcane ubi9 polyubiquitin
 PT gene promoter, useful for generating transgenic plants exhibiting
 PT important phenotypic properties, such as pest, disease and environmental
 PT stress resistance.
 XX PT
 XX Claim 1; SEQ ID NO 10; 79pp; English.
 XX PS
 XX The present invention provides nucleic acids having promoter activity.
 CC The invention is directed to isolating nucleic acid sequences from
 CC sugarcane polyubiquitin genes which are capable of directing constitutive
 CC expression of a nucleic acid of interest in monocotyledonous and
 CC dicotyledonous plants. The invention is useful in generating transgenic
 CC plants which exhibit commercially important phenotypic properties. The
 CC present sequence is sugarcane polyubiquitin ubi9 gene promoter DNA.
 XX
 XX Sequence 3688 BP; 844 A; 862 C; 925 G; 1055 T; 0 U; 2 Other;
 SQ
 Query Match 3.9%; Score 118.6; DB 12; Length 3688;
 Best Local Similarity 86.0%; Pred. No. 5.4e-22;

Matches 166; Conservative 0; Mismatches 24; Indels 3; Gaps 3;
 QY 1451 AGTTTCTAAGCCAGTCTCAGTGGGTTTCATCAGAGTTTCATGACATTAATAAGCT 1510
 |||||
 Db 1914 AGTTTCTGAGGCCCTCTCACT-GGATTTCATCAGAGTTTCATGACATTAATAAGCT 1856
 |||||
 QY 1511 GATGTGACACCGTATTGATGAAGAGAGAGATGATAAGAGTTTCATGCGAGTAGAGAGAGT 1570
 |||||
 Db 1855 GATGTGGCACCGTATTGATGAAGAGAGAGATGATAAGAGTTTCATGCGAATTAGAGAGAGT 1796
 |||||
 QY 1571 TTTCATGGGATGAACACTCTT-CTTCACCTGTTTCCAAAATAT-AGATGCAATTGGTAAGAGG 1628
 |||||
 Db 1795 TTTCAGGAAGATGAACACTCTTCTCGCACTGTTTCCAAAATATGGTTGCATTAAATACATG 1736
 |||||
 QY 1629 GCCATGAATCTC 1641
 |||||
 Db 1735 GCCATAAAATCCC 1723
 |||||
 RESULT 4
 AAZ28433/c
 ID AAZ28433 standard; DNA; 3691 BP.
 XX AC AAZ28433;
 XX 23-DEC-1999 (first entry)
 XX Ubi9 gene fragment including initiation codon and upstream sequence.
 DE XX
 XX Ubiquitin gene; ubi9; promoter; initiation codon; intron; monocotyledon;
 KW dicotyledon; disease resistance; environmental stress; sugar cane; ss.
 XX OS
 XX Saccharum sp.
 XX FH Key Location/Qualifiers
 FT TATA_signal /*tag= a
 FT 2201..2208
 FT 5'UTR /*tag= b
 FT 2249..2313
 FT WO9946976-A1.
 XX PN
 XX 23-SEP-1999.
 XX 18-MAR-1999; 99WO-US005985.
 XX 19-MAR-1998; 98US-0078768P.
 XX PR 17-MAR-1999; 99US-00270976.
 XX (UYHA-) UNIV HAWAII.
 XX (USDA) US DEPT OF AGRICULTURE.
 XX PI Albert HH, Wei H;
 XX WPI; 1999-590952/50.
 XX New nucleotide sequences derived from sugarcane polyubiquitin genes
 PT useful in regulating expression of nucleic acid sequences in
 PT monocotyledonous and dicotyledonous plants.
 XX PT
 XX Claim 1; Fig 7; 118pp; English.
 XX PS
 XX This sequence contains the sugar cane ubiquitin gene ubi9 initiation
 CC codon, and the upstream sequence of the gene including the 5'
 CC untranslated region. The gene has an intron immediately upstream of the
 CC initiation codon. The ubi9 gene is used in the invention as it has linked
 CC promoter activity, and the polyubiquitin genes are useful in regulating
 CC high expression of nucleic acid sequences in monocotyledonous and
 CC dicotyledonous plants. The nucleic acid sequences (ubi4 and ubi9) are
 CC used to create plants with commercially useful phenotypes. High levels of
 CC protein expression aid the generation of plants which exhibit
 CC commercially important phenotypic properties such as pest and disease
 CC resistance, resistance to environmental stress and improved qualities

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XX SQ Sequence 3691 BP; 845 A; 862 C; 927 G; 1055 T; 0 U; 2 Other;
Query Match 3.9%; Score 118.6; DB 2; Length 3691;
Best Local Similarity 86.0%; Pred. No. 5.4e-22;
Matches 166; Conservative 0; Mismatches 24; Indels 3; Gaps 3;
QY 1451 AGGTTTCTAAGCCAGTCTCAGTGGGGTTTCATCAGAGTTTCATGACATTAAATAAGCT 1510
DB 1914 AGTTTCTGAGCCCGTCTCAGT-GGATTTTCATCAGAGTTTCATGACATTAAATAGGCT 1856
QY 1511 GATGTGACACCGTATTGATGAAGAGAGAGATGAAGAGTTTCATGCGAGTAGAGAGAGT 1570
DB 1855 GATGTGGCACCCTATTGATGAAGAGAGAGATGAAGAGTTTCATGCGAATTAGAGAGAGT 1796
QY 1571 TTCATGGGGATGAACCTCTT-CTTCACCTGTTTCCAAATAT-AGATGCATTGGTAAGAGG 1628
DB 1795 TTTACGAAGATGAACCTCTTCTGCACTGTTTCCAAATATGCGTTCATTAATAACATG 1736
QY 1629 GCCATGAATCTC 1641
DB 1735 GCCATAAATCCC 1723

RESULT 5
ADK66205/c
ID ADK66205 standard; DNA; 3691 BP.
XX ADK66205;
AC ADK66205;
DT 06-MAY-2004 (first entry)
DE Sugarcane polyubiquitin ubi9 gene #1.
XX Polyubiquitin; monocotyledonous; dicotyledonous; transgenic plant;
KW phenotypic; sugarcane; plant; ds.
XX Saccharum sp.
FH Key Location/Qualifiers
FT misc_feature 1 /*tag= a
FT /note= "Upstream of 5' UTR"
FT 2249..2313 /*tag= b
FT intron 2314..3688 /*tag= c
FT
FT
XX US6686513-B1.
PD 03-FEB-2004.
XX 20-OCT-2000; 2000US-00693467.
PF 19-MAR-1998; 98US-0078767P.
PR 17-MAR-1999; 99US-00270976.
XX (USDA ) US SEC OF AGRIC.
PA (UTHA-) UNIV HAWAII.
PI Albert HH, Wei H;
XX WPI; 2004-106365/11.
XX New transgenic plant cell comprising the sugarcane ubi9 polyubiquitin
PT gene promoter, useful for generating transgenic plants exhibiting
PT important phenotypic properties, such as pest, disease and environmental
PT stress resistance.
XX Example 1; SEQ ID NO 3; 79pp; English.
PS The present invention provides nucleic acids having promoter activity.
XX The invention is directed to isolating nucleic acid sequences from
CC New nucleotide sequences derived from sugarcane polyubiquitin genes

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CC sugarcane polyubiquitin genes which are capable of directing constitutive
CC expression of a nucleic acid of interest in monocotyledonous and
CC dicotyledonous plants. The invention is useful in generating transgenic
CC plants which exhibit commercially important phenotypic properties. The
CC present sequence is sugarcane polyubiquitin ubi9 gene.
XX SQ Sequence 3691 BP; 845 A; 862 C; 927 G; 1055 T; 0 U; 2 Other;
Query Match 3.9%; Score 118.6; DB 12; Length 3691;
Best Local Similarity 86.0%; Pred. No. 5.4e-22;
Matches 166; Conservative 0; Mismatches 24; Indels 3; Gaps 3;
QY 1451 AGGTTTCTAAGCCAGTCTCAGTGGGGTTTCATCAGAGTTTCATGACATTAAATAAGCT 1510
DB 1914 AGTTTCTGAGCCCGTCTCAGT-GGATTTTCATCAGAGTTTCATGACATTAAATAGGCT 1856
QY 1511 GATGTGACACCGTATTGATGAAGAGAGAGATGAAGAGTTTCATGCGAGTAGAGAGAGT 1570
DB 1855 GATGTGGCACCCTATTGATGAAGAGAGAGATGAAGAGTTTCATGCGAATTAGAGAGAGT 1796
QY 1571 TTCATGGGGATGAACCTCTT-CTTCACCTGTTTCCAAATAT-AGATGCATTGGTAAGAGG 1628
DB 1795 TTTACGAAGATGAACCTCTTCTGCACTGTTTCCAAATATGCGTTCATTAATAACATG 1736
QY 1629 GCCATGAATCTC 1641
DB 1735 GCCATAAATCCC 1723

RESULT 6
AAZ28437/c
ID AAZ28437 standard; DNA; 5174 BP.
XX AAZ28437;
AC AAZ28437;
DT 23-DEC-1999 (first entry)
DE Sugar cane ubiquitin 9 (ubi9) gene.
XX Ubiquitin gene; ubi4; promoter; initiation codon; intron; monocotyledon;
KW dicotyledon; disease resistance; environmental stress; sugar cane; ss.
XX Saccharum sp.
FH Key Location/Qualifiers
FT CDS 3689..3691 /*tag= a
FT /product= "ubi9"
FT /note= "Ubiquitin 9 protein"
FT /transl_except= (Pos:4043..4045, aa:Xaa)
FT /transl_except= (Pos:4316..4318, aa:Xaa)
FT /transl_except= (Pos:4499..4501, aa:Xaa)
FT /transl_except= (Pos:4544..4547, aa:Xaa)
FT /note= "Xaa = Unknown"
XX WO9946976-A1.
XX 23-SEP-1999.
XX 18-MAR-1999; 99WO-US005985.
XX 19-MAR-1998; 98US-0078768P.
PR 17-MAR-1999; 99US-00270976.
XX (UTHA-) UNIV HAWAII.
PA (USDA ) US DEPT OF AGRICULTURE.
XX Albert HH, Wei H;
XX WPI; 1999-590952/50.
DR P-FSDB; AAY43047.
XX New nucleotide sequences derived from sugarcane polyubiquitin genes

```


CC disease resistance (e.g. to insect infestation, fungal disease, bacterial
 CC infection, Goss' Bacterial Wilt, blight, Stewart's bacterial Wilt, Holcus
 CC spot, bacterial leaf blight, leaf spot, bacterial stripe and maize dwarf
 CC mosaic virus infection) and resistance to environmental stress (e.g.
 CC water stress, pH stress, temperature stress, pollution, injury or
 CC pesticides. The present sequence is cdp cDNA sequence.
 XX
 SQ Sequence 290 BP; 58 A; 113 C; 75 G; 43 T; 0 U; 1 Other;

Query Match 2.0%; Score 61.2; DB 7; Length 290;
 Best Local Similarity 71.1%; Pred. No. 2.1e-06;
 Matches 81; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 2903 AGCCGTGCGCCATGGCGTTCAGCAAGGAGCACACACAGCACTCATCAGCAGGCGGTGC 2962
 |||||
 DB 10 ACCAATAGCCCATGGTTCATCTGGAGCAAGCTGCACACAGCATCGCAGGCGGTGC 69

QY 2963 TGGATGCTCAGCTCAGCTTGGACACACACCTGGCTATGTCAGTCCATGG 3016
 |||||
 DB 70 TCGAGCTCAGCTCAGCTTGGACACACAGCTTGGCTTTCATCAAGTCCATGG 123

RESULT 12
 ADA72001/c
 ID ADA72001 standard; DNA; 2000 BP.

AC ADA72001;
 XX
 DT 20-NOV-2003 (first entry)

XX Rice gene, SEQ ID 5326.
 XX Plant; bacterial infection; fungal infection; viral infection; rice;
 KW gene; db.
 XX

OS Oryza sativa.
 XX
 PN WO2003000898-A1.
 XX

PD 03-JAN-2003.
 XX
 PF 22-JUN-2001; 2001WO-IB001105.
 XX

PR 22-JUN-2001; 2001WO-IB001105.
 XX
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
 PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
 XX WPI; 2003-175290/17.

XX Identifying at least one gene involved in plant resistance or response to
 PT pathogenic infection for conferring resistance or tolerance to a plant to
 PT bacterial, fungal or viral infection by determining or detecting plant
 PT gene expression.
 XX

PS Claim 27; SEQ ID NO 5326; 899pp; English.
 XX The present invention relates to a method (M1) for identifying genes
 CC involved in plant resistance or response to pathogenic infection. M1
 CC comprises identifying a gene whose expression is significantly altered in
 CC the incompatible interaction of plant gene expression relative to
 CC expression of the gene in an uninfected plant, in a mutant plant that
 CC does not express a gene associated with response to pathogenic infection,
 CC or in a corresponding incompatible or compatible interaction. (M1) is
 CC useful for conferring resistance to resistance or tolerance to a plant to
 CC bacterial, fungal or viral infection. The present sequence was used to
 CC illustrate the invention.

SQ Sequence 2000 BP; 708 A; 348 C; 340 G; 604 T; 0 U; 0 Other;
 XX

Query Match 2.0%; Score 60.4; DB 8; Length 2000;

Best Local Similarity 62.7%; Pred. No. 1.1e-05;
 Matches 94; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 2431 AAGTCGACCACCAACATAAGAGTTAAATGATGGTAGGCTCTTGATCTTGTCTGG 2490
 |||||
 DB 706 AAGTTCCTCTCAAAAAAAACTTTAGACTAAAGTGCATGGGTGGTCCATAAAACTTGTACGG 647

QY 2491 AGGTGCCACTTAGGTCCACAACTCTCAAAATGCAATTTTGACACCCCTAAATGTTATTCAA 2550
 |||||
 DB 646 GTGTGTACCTACGTCCATAAACTCTTAAATGTTATTTTGGATCCGTCGTAATCTC 587

QY 2551 GTGTGCCACTTAGATCTACAAACTCTCAAA 2580
 |||||
 DB 586 GGGTGTATGTGGGTCTAAATGGGCTCAA 557

RESULT 13
 ADC08563/c
 ID ADC08563 standard; DNA; 2010 BP.

AC ADC08563;
 XX
 DT 18-DEC-2003 (first entry)

XX Rice DNA sequence Seq ID868 related to grain filling.

XX plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;
 KW carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;
 KW tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet;
 KW wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain;
 KW gene; db; plant.

OS Oryza sativa.

XX WO2003000905-A2.

XX 03-JAN-2003.

XX 21-JUN-2002; 2002WO-IB002450.

XX 22-JUN-2001; 2001US-0300112P.

PR 26-SEP-2001; 2001US-0325277P.

PR 20-DEC-2001; 2001US-0342327P.

XX (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Zhu T, Cheng W, Briggs S, Cooper B, Goff SA, Moughamer T;
 PI Glazebrook J, Katagiri F, Kreps J, Provart N, Ricke D;
 XX WPI; 2003-229341/22.

XX New plant genes encoding polypeptides having an activity involved in or
 PT associated with the synthesis, metabolism or degradation of carbohydrates
 PT in the plant grain useful in generating plants having improved
 PT nutritional properties.

PS Disclosure; SEQ ID NO 868; 130pp; English.

XX This invention, in the area of plant biotechnology, relates to novel
 CC polynucleotides comprising a nucleotide sequence encoding a protein which
 CC is involved in or associated with the synthesis, metabolism or
 CC degradation of carbohydrates in the plant grain and the expression of
 CC which is up-regulated during grain filling. The plant is selected from
 CC corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco,
 CC sugarbeet, wheat, and rice. The invention may be useful for the
 CC improvement of protein, oil, starch, fibre and moisture content of the
 CC cereal grains. In addition, carbohydrate levels may be modified to a more
 CC desirable level using the present invention. The present sequence is a
 CC DNA sequence of a rice gene promoter. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WPIO at
 CC ftp.wipo.int/pub/publishedpct_sequences.

SQ Sequence 2010 BP; 563 A; 472 C; 389 G; 586 T; 0 U; 0 Other;

Query Match 2.0%; Score 59; DB 10; Length 2010;
 Best Local Similarity 58.0%; Pred. No. 2.7e-05;
 Matches 141; Conservative 0; Mismatches 100; Indels 2; Gaps 2;

QY 2434 TCGACACACACCAACATAAAGAGTTAAATGCATGGTAGGCTCTTGATCTTCTGCTGGAGG 2493
 Db 918 TCTTCATATCGCAAGTAATAATAGTAGTGACGGCGGTCTTAAACTTGTAGGGGTG 859

QY 2494 TGGCACTTAGGTCCACAACTCTCAAATTCGCAATTTTGGACCCCTAAATGTTATTCAGAGTG 2553
 Db 858 TGTCAATTAGGTCCCTAAACTCTCAAATTCGCAATTCGCAAGTCCGAGAACTTGTATAGTG 799

QY 2554 TGGCACTTAGGTACAACTCTCAAATTCGCAATTTTGGACCCCTAAATGTTATTCAGAGTG 2613
 Db 798 TATCATCTAGGT-TCCAAATCGCCACACCCCTTCAGGATCTATGTGCAATGATGTGG 740

QY 2614 TGTCACTTAGGCAAGAAAGTTAGATAATTTTGA-TAAGCTATGGACCAAAATTAATTTA 2672
 Db 739 CATGCCACATGGACATGACGTGGTATTTTGAAGTACGCAAAATGGACCAATTAATTTT 680

QY 2673 TGT 2675
 Db 679 TTT 677

RESULT 14
 ADJ41371
 ID ADJ41371 standard; cDNA; 2000 BP.
 AC ADJ41371;
 DT 06-MAY-2004 (first entry)
 XX Plant cDNA #2371.
 DE
 KW plant; gene; ss; transcription; plant genome augmentation; cereal;
 KW soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet;
 KW maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance;
 KW stress tolerance; salt tolerance; cold tolerance; drought tolerance;
 KW plant nutrition; apical dominance; dwarfism; early flowering; antiviral;
 KW antifungal.
 XX Eukaryota.
 OS
 XX US2004016025-AL.
 PN
 XX 22-JAN-2004.
 PD
 XX 26-SEP-2002; 2002US-00260238.
 PF
 XX 26-SEP-2001; 2001US-0325277P.
 PR 26-SEP-2001; 2001US-0325448P.
 PR 04-APR-2002; 2002US-0370620P.
 XX (BUDW/) BUDWORTH P.
 PA (MOUG/) MOUGHAMER T.
 PA (BRIG/) BRIGGS S F.
 PA (COOP/) COOPER B.
 PA (GLAZ/) GLAZEBOOK J.
 PA (GOFF/) GOFF S A.
 PA (KATA/) KATAGIRI F.
 PA (KREP/) KREPS J.
 PA (PROV/) PROVART N.
 PA (RICK/) RICHE D.
 PA (ZHUT/) ZHU T.
 XX Budworth P, Moughamer T, Briggs SP, Cooper B, Glazebrook J;
 PI Goff SA, Katagiri F, Kreps J, Provart N, Ricke D, Zhu T;
 XX WPI; 2004-190374/18.
 DR
 XX

PT New rice promoter, useful for manipulating crop plants to alter or
 PT improve phenotypic characteristics, e.g. produce large quantities of oil
 PT or proteins, resistance to insecticides, virus or fungi, stress tolerance
 PT or high nutritional value.
 XX
 PS Claim 1; SEQ ID NO 2371; 230pp; English.
 XX
 CC The invention relates to plant nucleotide sequences that direct seed-,
 CC leaf- and/or stem-, panicle-, root- or pollen-specific or -preferential
 CC or constitutive transcription of an operatively linked nucleic acid
 CC segment. The invention also relates to a method for augmenting a plant
 CC genome and a method of identifying a gene, where its expression is
 CC altered in the seed, leaf, stem, panicle, pollen, root or is constitutive
 CC in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower,
 CC canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley,
 CC sorghum, rice or wheat. The polynucleotides and the polypeptides they
 CC encode are useful for manipulating crop plants to alter or improve
 CC phenotypic characteristics, to produce large quantities of oil or
 CC proteins, to incur resistance to insecticides, viruses or fungi, and to
 CC incur stress tolerance (e.g. salt, cold or drought) to ensure the plants
 CC have a high nutritional value with reduced apical dominance or dwarfism,
 CC early flowering or altered metabolic pathways. This sequence represents a
 CC plant nucleic acid of the invention. Note: The sequence data for this
 CC patent did not form part of the printed specification but was obtained in
 CC electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.
 XX
 SQ Sequence 2000 BP; 662 A; 359 C; 368 G; 609 T; 0 U; 2 Other;

Query Match 1.9%; Score 57.6; DB 12; Length 2000;
 Best Local Similarity 56.2%; Pred. No. 6.7e-05;
 Matches 108; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 2448 ACATAAGAGTTAAATGCATGGTAGGCTCTTGATCTTGTCTGGAGTGCCACTAGGTCC 2507
 Db 885 AAAAATAGAGTAAAGTCCATCACCGGTCCCTAAAACCTTGTTGTTGTCATCGCGGTCC 944

QY 2508 ACAAACTCTCAAATTCGCAATTTTTCACACCCCTAAATGTTATTCAGTGTCCTAGATGCT 2567
 Db 945 CTAACCTCGCAATTCACCGTTCAGGTCTCAAACTTGTCAATGTTGTCATCCGGTCC 1004

QY 2568 ACAAACTCTCAAATTCGCAATTTTTCATACCCCTAGTGTGTTTCAAGTGTGTCATAGGCAA 2627
 Db 1005 CTAACCTTACAGATCACTCGTTTAGTCTCTCAAACTTGTTCAGTGTGTCACCCCGGTCT 1064

QY 2628 GAAAGTTAGAT 2639
 Db 1065 CTAACCTTGGAT 1076

RESULT 15
 ADC08563
 ID ADC08563 standard; DNA; 2010 BP.
 XX
 AC ADC08563;
 XX
 DT 18-DEC-2003 (first entry)
 DE
 XX Rice DNA sequence Seq ID868 related to grain filling.
 XX
 KW plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;
 KW carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;
 KW tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet;
 KW wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain;
 KW gene; ds; plant.
 XX
 OS Oryza sativa.
 XX
 XX WO200300905-A2.
 PN
 XX 03-JAN-2003.
 PD
 XX 21-JUN-2002; 2002WO-IB002450.
 PF
 XX

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OM nucleic - nucleic search, using sw model

Run on: February 16, 2005, 02:54:17 ; Search time 490 seconds
(without alignments)
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	118.6	3.9	3688	4	US-09-866-153-10
C 2	118.6	3.9	3688	4	US-09-693-467A-10
C 3	118.6	3.9	3688	4	US-09-270-976-10
C 4	118.6	3.9	3691	4	US-09-866-153-3
C 5	118.6	3.9	3691	4	US-09-693-467A-3
C 6	118.6	3.9	3691	4	US-09-270-976-3
C 7	118.6	3.9	5174	4	US-09-866-153-8
C 8	118.6	3.9	5174	4	US-09-693-467A-8
C 9	118.6	3.9	5174	4	US-09-270-976-8
C 10	49.4	1.6	1141	4	US-09-806-708B-22
C 11	46	1.5	1141	4	US-09-806-708B-22
C 12	44	1.5	832	4	US-09-621-976-2813
C 13	41.2	1.4	832	4	US-09-621-976-2813
C 14	40.8	1.4	601	4	US-09-949-016-150744
C 15	40.8	1.4	294836	4	US-09-949-016-15974
C 16	40.2	1.3	4467	2	US-08-565-907A-1
C 17	40.2	1.3	4467	2	US-08-910-551B-1
C 18	40.2	1.3	4467	2	US-08-909-425A-1
C 19	39.4	1.3	1677	2	US-08-684-101-1
C 20	39.4	1.3	1677	2	US-09-205-814-1
C 21	39.4	1.3	7218	1	US-08-232-463-14
C 22	39.2	1.3	636	3	US-08-998-416-1137
C 23	39	1.3	505	4	US-09-621-976-15639
C 24	39	1.3	601	4	US-09-949-016-107633
C 25	39	1.3	837	3	US-08-998-416-288
C 26	39	1.3	390890	4	US-09-949-016-14720
C 27	38.6	1.3	4253	4	US-08-956-171E-118

28	38.6	1.3	4253	4	US-08-781-986A-118	Sequence 118, Appl
29	38.4	1.3	2755	3	US-08-749-522-2	Sequence 2, Appli
C 30	38.4	1.3	19480	4	US-09-949-016-14095	Sequence 14095, A
C 31	38.4	1.3	387902	4	US-09-949-016-14543	Sequence 14543, A
C 32	38.4	1.3	421883	4	US-09-949-016-12557	Sequence 12557, A
C 33	38	1.3	17633	4	US-09-949-016-13137	Sequence 13137, A
C 34	37.6	1.2	1113	4	US-09-248-796A-9644	Sequence 9644, Ap
C 35	37.4	1.2	2287	3	US-08-845-258-8	Sequence 8, Appli
C 36	37.4	1.2	2287	3	US-08-990-571-8	Sequence 8, Appli
C 37	37.4	1.2	2287	3	US-08-723-142A-8	Sequence 8, Appli
C 38	37.4	1.2	2287	3	US-09-528-784A-8	Sequence 8, Appli
C 39	37.4	1.2	2287	4	US-09-569-098A-8	Sequence 8, Appli
C 40	37.4	1.2	38575	4	US-09-949-016-12876	Sequence 12876, A
C 41	37.4	1.2	38575	4	US-09-949-016-13871	Sequence 13871, A
C 42	37.2	1.2	2430	3	US-08-845-258-3	Sequence 3, Appli
C 43	37.2	1.2	2430	3	US-08-845-258-40	Sequence 40, Appl
C 44	37.2	1.2	2430	3	US-08-990-571-3	Sequence 3, Appli
C 45	37.2	1.2	2430	3	US-08-990-571-40	Sequence 40, Appl

ALIGNMENTS

RESULT 1
US-09-866-153-10/c
; Sequence 10, Application US/09866153
; Patent No. 6638766
; GENERAL INFORMATION:
; APPLICANT: Albert, Henrik H.
; APPLICANT: Wei, Hairong
; TITLE OF INVENTION: PLANT PROMOTER SEQUENCES AND METHODS OF USE THEREOF
; FILE REFERENCE: US-03648
; CURRENT APPLICATION NUMBER: US/09/866,153
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 09/270,976
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 3688
; TYPE: DNA
; ORGANISM: Saccharum Hybrid Cultivar 32-8560
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (9)
; OTHER INFORMATION: The "n" at position 9 is any nucleotide.
US-09-866-153-10

Query Match	3.9%	Score 118.6;	DB 4;	Length 3688;
Best Local Similarity	86.0%	Pred. No. 1.3e-25;		
Matches 166;	Conservative 0;	Mismatches 24;	Indels 3;	Gaps 3;
QY	1451	AGTTTCTTAAGCCAGTCTCAGTGGGGTTTCATCAGAGTTTCATGAGCATTAAATAGCT	1510	
Db	1914	AGTTTCTTGAAGCCCGCTCTCAGT-GGATTTCATCAGAGTTTCATGAGCATTAAATAGCT	1856	
QY	1511	GATGTGACACCGTATTGATGAAGAGAGATGAATGAAGTTTCATGCCAGTAGAGAGT	1570	
Db	1855	GATGTGACACCGTATTGATGAAGAGAGATGAATGAAGTTTCATGCCAGTAGAGAGT	1796	
QY	1571	TTTCATGGGGATGAACACTCTT-CCTTCACCTGTTTCCAAAATAT-AGATGCATTGGTAAAGG	1628	
Db	1795	TTTACGAAGATGAACCTCTCTCTGCACCTGTTTCCAAATATGGGTTGCATTAAATACATG	1736	
QY	1629	GCCATGAATCTC	1641	
Db	1735	GCCATAAATCCC	1723	

RESULT 2
US-09-693-467A-10/c
; Sequence 10, Application US/09693467A
; Patent No. 6686513

GENERAL INFORMATION:
; APPLICANT: Albert, Henrik H.
; APPLICANT: Wei, Hairong
; TITLE OF INVENTION: PLANT PROMOTER SEQUENCES AND METHODS OF USE THEREOF
; FILE REFERENCE: US-04331
; CURRENT APPLICATION NUMBER: US/09/693,467A
; CURRENT FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/270,976
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 3688
; TYPE: DNA
; ORGANISM: Saccharum Hybrid Cultivar 32-8560
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (9)
; OTHER INFORMATION: The "n" at position 9 is any nucleotide.
US-09-693-467A-10
Query Match 3.9%; Score 118.6; DB 4; Length 3688;
Best Local Similarity 86.0%; Pred. No. 1.3e-25;
Matches 166; Conservative 0; Mismatches 24; Indels 3; Gaps 3;
QY 1451 AGTTTCTAAGCCAGTCTCAGTGGGTTTCATCAGAGTTTCATGACATTAATAAGCT 1510
DB 1914 AGTTTCTGAGGCCGCTCTCAGT-GGATTTTCATCAGAGTTTCATGACATTAATAAGCT 1856
QY 1511 GATGTGACACCGTATTGATGAAGAGAGATGATGAAGAGTTTCATGCGAGTAGAGAGT 1570
DB 1855 GATGTGACACCGTATTGATGAAGAGAGATGATGAAGAGTTTCATGCGAGTAGAGAGT 1796
QY 1571 TTTCATGGGATGAAACTCTT-CTTCACCTGTTTCCAAATAT-AGATGCAATGGTAAGAGG 1628
DB 1795 TTTCACGAAGATGAAACTCTTCTCGCACTGTTTCCAAATATGGTGTGCAATTAATAACATG 1736
QY 1629 GCCATGAATCTC 1641
DB 1735 GCCATAAATCCC 1723

RESULT 3
US-09-270-976-10/c
; Sequence 10, Application US/09270976A
; Patent No. 6706948
; GENERAL INFORMATION:
; APPLICANT: Albert, Henrik H.
; APPLICANT: Wei, Hairong
; TITLE OF INVENTION: PLANT PROMOTER SEQUENCES AND METHODS OF USE THEREOF
; FILE REFERENCE: US-03648
; CURRENT APPLICATION NUMBER: US/09/270,976A
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 3688
; TYPE: DNA
; ORGANISM: Saccharum Hybrid Cultivar 32-8560
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (9)
; OTHER INFORMATION: The "n" at position 9 is any nucleotide.
US-09-270-976-10
Query Match 3.9%; Score 118.6; DB 4; Length 3688;
Best Local Similarity 86.0%; Pred. No. 1.3e-25;
Matches 166; Conservative 0; Mismatches 24; Indels 3; Gaps 3;
QY 1451 AGTTTCTAAGCCAGTCTCAGTGGGTTTCATCAGAGTTTCATGACATTAATAAGCT 1510
DB 1914 AGTTTCTGAGGCCGCTCTCAGT-GGATTTTCATCAGAGTTTCATGACATTAATAAGCT 1856

QY 1511 GATGTGACACCGTATTGATGAAGAGAGATGATGAAGAGTTTCATGCGAGTAGAGAGT 1570
DB 1855 GATGTGACACCGTATTGATGAAGAGAGATGATGAAGAGTTTCATGCGAGTAGAGAGT 1796
QY 1571 TTTCATGGGATGAAACTCTT-CTTCACCTGTTTCCAAATAT-AGATGCAATGGTAAGAGG 1628
DB 1795 TTTCACGAAGATGAAACTCTTCTCGCACTGTTTCCAAATATGGTGTGCAATTAATAACATG 1736
QY 1629 GCCATGAATCTC 1641
DB 1735 GCCATAAATCCC 1723
RESULT 4
US-09-866-153-3/c
; Sequence 3, Application US/09866153
; Patent No. 6638766
; GENERAL INFORMATION:
; APPLICANT: Albert, Henrik H.
; APPLICANT: Wei, Hairong
; TITLE OF INVENTION: PLANT PROMOTER SEQUENCES AND METHODS OF USE THEREOF
; FILE REFERENCE: US-03648
; CURRENT APPLICATION NUMBER: US/09/866,153
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 09/270,976
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 3691
; TYPE: DNA
; ORGANISM: Saccharum Hybrid Cultivar H32-8560
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (9)
; OTHER INFORMATION: The "n" at position 9 is any nucleotide.
; NAME/KEY: misc_feature
; LOCATION: (3613)
; OTHER INFORMATION: The "n" at position 3613 is any nucleotide.
US-09-866-153-3
Query Match 3.9%; Score 118.6; DB 4; Length 3691;
Best Local Similarity 86.0%; Pred. No. 1.3e-25;
Matches 166; Conservative 0; Mismatches 24; Indels 3; Gaps 3;
QY 1451 AGTTTCTAAGCCAGTCTCAGTGGGTTTCATCAGAGTTTCATGACATTAATAAGCT 1510
DB 1914 AGTTTCTGAGGCCGCTCTCAGT-GGATTTTCATCAGAGTTTCATGACATTAATAAGCT 1856
QY 1511 GATGTGACACCGTATTGATGAAGAGAGATGATGAAGAGTTTCATGCGAGTAGAGAGT 1570
DB 1855 GATGTGACACCGTATTGATGAAGAGAGATGATGAAGAGTTTCATGCGAGTAGAGAGT 1796
QY 1571 TTTCATGGGATGAAACTCTT-CTTCACCTGTTTCCAAATAT-AGATGCAATGGTAAGAGG 1628
DB 1795 TTTCACGAAGATGAAACTCTTCTCGCACTGTTTCCAAATATGGTGTGCAATTAATAACATG 1736
QY 1629 GCCATGAATCTC 1641
DB 1735 GCCATAAATCCC 1723

RESULT 5
US-09-693-467A-3/c
; Sequence 3, Application US/09693467A
; Patent No. 6686513
; GENERAL INFORMATION:
; APPLICANT: Albert, Henrik H.
; APPLICANT: Wei, Hairong
; TITLE OF INVENTION: PLANT PROMOTER SEQUENCES AND METHODS OF USE THEREOF
; FILE REFERENCE: US-04331
; CURRENT APPLICATION NUMBER: US/09/693,467A
; CURRENT FILING DATE: 2000-10-20
Query Match 3.9%; Score 118.6; DB 4; Length 3691;
Best Local Similarity 86.0%; Pred. No. 1.3e-25;
Matches 166; Conservative 0; Mismatches 24; Indels 3; Gaps 3;
QY 1451 AGTTTCTAAGCCAGTCTCAGTGGGTTTCATCAGAGTTTCATGACATTAATAAGCT 1510
DB 1914 AGTTTCTGAGGCCGCTCTCAGT-GGATTTTCATCAGAGTTTCATGACATTAATAAGCT 1856
QY 1511 GATGTGACACCGTATTGATGAAGAGAGATGATGAAGAGTTTCATGCGAGTAGAGAGT 1570
DB 1855 GATGTGACACCGTATTGATGAAGAGAGATGATGAAGAGTTTCATGCGAGTAGAGAGT 1796
QY 1571 TTTCATGGGATGAAACTCTT-CTTCACCTGTTTCCAAATAT-AGATGCAATGGTAAGAGG 1628
DB 1795 TTTCACGAAGATGAAACTCTTCTCGCACTGTTTCCAAATATGGTGTGCAATTAATAACATG 1736
QY 1629 GCCATGAATCTC 1641
DB 1735 GCCATAAATCCC 1723


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; PRIOR APPLICATION NUMBER: 09/270,976
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 3691
; TYPE: DNA
; ORGANISM: Saccharum Hybrid Cultivar H32-8560
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (9)
; OTHER INFORMATION: The "n" at position 9 is any nucleotide.
; NAME/KEY: misc_feature
; LOCATION: (3613)
; OTHER INFORMATION: The "n" at position 3613 is any nucleotide.
US-09-693-467A-3

Query Match      3.9%; Score 118.6; DB 4; Length 3691;
Best Local Similarity 86.0%; Pred. No. 1.3e-25;
Matches 166; Conservative 0; Mismatches 24; Indels 3; Gaps 3;

QY 1451 AGTTTCTTAAGCCAGTCTCAGTGGGTTTCATCAGAGTTCATGACATTAAATAAGCT 1510
DB 1914 AGTTTCTGAGCCCGTCTCAGT-GGATTTTCATCAGAGTTCATGACATTAAATAGCT 1856

QY 1511 GATGTGACACCGTATTGATGAAGAGAGATGATAAGAGTTCATGCGAGTAGAGAGT 1570
DB 1855 GATGTGGCACCCTATTGATGAAGAGAGAGATGATAAGAGTTCATGCGAATTAGAGAGT 1796

QY 1629 GCCATGAATCTC 1641
DB 1735 GCCATAAAATCCC 1723

RESULT 6
US-09-270-976-3/c
; Sequence 3, Application US/09270976A
; Patent No. 6706948
; GENERAL INFORMATION:
; APPLICANT: Albert, Henrik H.
; APPLICANT: Wei, Hairong
; TITLE OF INVENTION: PLANT PROMOTER SEQUENCES AND METHODS OF USE THEREOF
; FILE REFERENCE: UH-03648
; CURRENT APPLICATION NUMBER: US/09/270,976A
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 3691
; TYPE: DNA
; ORGANISM: Saccharum Hybrid Cultivar H32-8560
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (9)
; OTHER INFORMATION: The "n" at position 9 is any nucleotide.
; NAME/KEY: misc_feature
; LOCATION: (3613)
; OTHER INFORMATION: The "n" at position 3613 is any nucleotide.
US-09-270-976-3

Query Match      3.9%; Score 118.6; DB 4; Length 3691;
Best Local Similarity 86.0%; Pred. No. 1.3e-25;
Matches 166; Conservative 0; Mismatches 24; Indels 3; Gaps 3;

QY 1451 AGTTTCTTAAGCCAGTCTCAGTGGGTTTCATCAGAGTTCATGACATTAAATAAGCT 1510
DB 1914 AGTTTCTGAGCCCGTCTCAGT-GGATTTTCATCAGAGTTCATGACATTAAATAGCT 1856

QY 1511 GATGTGACACCGTATTGATGAAGAGAGATGATAAGAGTTCATGCGAGTAGAGAGT 1570
DB 1855 GATGTGGCACCCTATTGATGAAGAGAGAGATGATAAGAGTTCATGCGAATTAGAGAGT 1796

QY 1629 GCCATGAATCTC 1641
DB 1735 GCCATAAAATCCC 1723

RESULT 7
US-09-866-153-8/c
; Sequence 8, Application US/09866153
; Patent No. 6638766
; GENERAL INFORMATION:
; APPLICANT: Albert, Henrik H.
; APPLICANT: Wei, Hairong
; TITLE OF INVENTION: PLANT PROMOTER SEQUENCES AND METHODS OF USE THEREOF
; FILE REFERENCE: UH-03648
; CURRENT APPLICATION NUMBER: US/09/866,153
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 09/270,976
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 5174
; TYPE: DNA
; ORGANISM: Saccharum Hybrid Cultivar H32-8560
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (9)
; OTHER INFORMATION: The "n" at position 9 is any nucleotide.
; NAME/KEY: misc_feature
; LOCATION: (4318)
; OTHER INFORMATION: The "n" at position 4318 is any nucleotide.
; NAME/KEY: misc_feature
; LOCATION: (4546)
; OTHER INFORMATION: The "n" at position 4546 is any nucleotide.
; NAME/KEY: misc_feature
; LOCATION: (4890)
; OTHER INFORMATION: The "n" at position 4890 is any nucleotide.
; NAME/KEY: misc_feature
; LOCATION: (5117)
; OTHER INFORMATION: The "n" at position 5117 is any nucleotide.
; NAME/KEY: misc_feature
; LOCATION: (5125)
; OTHER INFORMATION: The "n" at position 5125 is any nucleotide.
; NAME/KEY: misc_feature
; LOCATION: (5150)
; OTHER INFORMATION: The "n" at position 5150 is any nucleotide.
US-09-866-153-8

Query Match      3.9%; Score 118.6; DB 4; Length 5174;
Best Local Similarity 86.0%; Pred. No. 1.6e-25;
Matches 166; Conservative 0; Mismatches 24; Indels 3; Gaps 3;

QY 1451 AGTTTCTTAAGCCAGTCTCAGTGGGTTTCATCAGAGTTCATGACATTAAATAAGCT 1510
DB 1914 AGTTTCTGAGCCCGTCTCAGT-GGATTTTCATCAGAGTTCATGACATTAAATAGCT 1856

QY 1511 GATGTGACACCGTATTGATGAAGAGAGATGATAAGAGTTCATGCGAGTAGAGAGT 1570
DB 1855 GATGTGGCACCCTATTGATGAAGAGAGAGATGATAAGAGTTCATGCGAATTAGAGAGT 1796

QY 1571 TTCATGGGATGAAACTCTT-CTTCACGTGTTTCCAAAATAT-AGATGCAATTGGTAAGAGG 1628
DB 1795 TTTACGAAGATGAAACTCTTCCTGCACTGTTTCCAAAATATGGGTTGCATTAAATACATG 1736

Query Match      3.9%; Score 118.6; DB 4; Length 3691;
Best Local Similarity 86.0%; Pred. No. 1.3e-25;
Matches 166; Conservative 0; Mismatches 24; Indels 3; Gaps 3;

QY 1451 AGTTTCTTAAGCCAGTCTCAGTGGGTTTCATCAGAGTTCATGACATTAAATAAGCT 1510
DB 1914 AGTTTCTGAGCCCGTCTCAGT-GGATTTTCATCAGAGTTCATGACATTAAATAGCT 1856

QY 1511 GATGTGACACCGTATTGATGAAGAGAGATGATAAGAGTTCATGCGAGTAGAGAGT 1570
DB 1855 GATGTGGCACCCTATTGATGAAGAGAGAGATGATAAGAGTTCATGCGAATTAGAGAGT 1796

QY 1629 GCCATGAATCTC 1641
DB 1735 GCCATAAAATCCC 1723
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QY 1629 GCATGAATCTC 1641
Db 1735 GCATAAATCCC 1723

RESULT 8

US-09-693-467A-8/c

; Sequence 8, Application US/09693467A

; Patent No. 668513

; GENERAL INFORMATION:

; APPLICANT: Albert, Henrik H.

; APPLICANT: Wei, Hairong

; TITLE OF INVENTION: PLANT PROMOTER SEQUENCES AND METHODS OF USE THEREOF

; FILE REFERENCE: UH-04331

; CURRENT APPLICATION NUMBER: US/09/693,467A

; CURRENT FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 09/270,976

; PRIOR FILING DATE: 1999-03-17

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 8

; LENGTH: 5174

; TYPE: DNA

; ORGANISM: Saccharum Hybrid Cultivar H32-8560

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (9)

; OTHER INFORMATION: The "n" at position 9 is any nucleotide.

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (4318)

; OTHER INFORMATION: The "n" at position 4318 is any nucleotide.

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (4546)

; OTHER INFORMATION: The "n" at position 4546 is any nucleotide.

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (4890)

; OTHER INFORMATION: The "n" at position 4890 is any nucleotide.

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (5117)

; OTHER INFORMATION: The "n" at position 5117 is any nucleotide.

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (5125)

; OTHER INFORMATION: The "n" at position 5125 is any nucleotide.

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (5150)

; OTHER INFORMATION: The "n" at position 5150 is any nucleotide.

; US-09-693-467A-8

Query Match

Best Local Similarity 3.9%; Score 118.6; DB 4; Length 5174;

Matches 166; Conservative 0; Mismatches 24; Indels 3; Gaps 3;

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Db 1914 AGTTTCTGAGCCCGTCTCAGT-GGATTTTCATCAGAGTTTCATCGACATTAATAAGCT 1856

QY 1511 GATGTGACACCGTATTGATGAAGAGAGATGAAGAGTTTCATCGAGTAGAGAGT 1570

Db 1855 GATGTGACACCGTATTGATGAAGAGAGATGAAGAGTTTCATCGAGTAGAGAGT 1796

QY 1571 TTTCATGGGATGAACCTCTT-CTTCACCTGTTTCCAAATAT-AGATGCATTGGTAAGAGG 1628

Db 1795 TTTCATGGGATGAACCTCTTCTCTGACCTGTTTCCAAATATGGGTTCATTAAATACATG 1736

QY 1629 GCATGAATCTC 1641

Db 1735 GCATAAATCCC 1723

RESULT 9

US-09-270-976-8/c

; Sequence 8, Application US/09270976A

; Patent No. 6706948

; GENERAL INFORMATION:

; APPLICANT: Albert, Henrik H.

; APPLICANT: Wei, Hairong

; TITLE OF INVENTION: PLANT PROMOTER SEQUENCES AND METHODS OF USE THEREOF

; FILE REFERENCE: UH-03648

; CURRENT APPLICATION NUMBER: US/09/270,976A

; CURRENT FILING DATE: 1999-03-17

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 8

; LENGTH: 5174

; TYPE: DNA

; ORGANISM: Saccharum Hybrid Cultivar H32-8560

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (9)

; OTHER INFORMATION: The "n" at position 9 is any nucleotide.

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (4318)

; OTHER INFORMATION: The "n" at position 4318 is any nucleotide.

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (4546)

; OTHER INFORMATION: The "n" at position 4546 is any nucleotide.

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (4890)

; OTHER INFORMATION: The "n" at position 4890 is any nucleotide.

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (5117)

; OTHER INFORMATION: The "n" at position 5117 is any nucleotide.

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (5125)

; OTHER INFORMATION: The "n" at position 5125 is any nucleotide.

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (5150)

; OTHER INFORMATION: The "n" at position 5150 is any nucleotide.

; US-09-270-976-8

Query Match

Best Local Similarity 3.9%; Score 118.6; DB 4; Length 5174;

Matches 166; Conservative 0; Mismatches 24; Indels 3; Gaps 3;

QY 1451 AGTTTCTAAGCCGAGTCTCAGTGGGGTTTCATCAGAGTTTCATCGACATTAATAAGCT 1510

Db 1914 AGTTTCTGAGCCCGTCTCAGT-GGATTTTCATCAGAGTTTCATCGACATTAATAAGCT 1856

QY 1511 GATGTGACACCGTATTGATGAAGAGAGATGAAGAGTTTCATCGAGTAGAGAGT 1570

Db 1855 GATGTGACACCGTATTGATGAAGAGAGATGAAGAGTTTCATCGAGTAGAGAGT 1796

QY 1571 TTTCATGGGATGAACCTCTT-CTTCACCTGTTTCCAAATAT-AGATGCATTGGTAAGAGG 1628

Db 1795 TTTCATGGGATGAACCTCTTCTCTGACCTGTTTCCAAATATGGGTTCATTAAATACATG 1736

QY 1629 GCATGAATCTC 1641

Db 1735 GCATAAATCCC 1723

RESULT 10

US-09-806-708B-22

; Sequence 22, Application US/09806708B

[illegible]


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US-09-949-016-150744
; Sequence 150744, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 150744
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-150744

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QY	1258	AAATTGTACHTTTAGTTGTTTGACATGAAGCTCGAACTATGAATTTATGATGATTTGT	1317		
DB	110	AGAAAGTACATTTTACATTCCTATCAAAAAATATATGAATGATGACTTTCTCTCGATTCC	169		
QY	1318	GGCTTGTGAGCTACTCCGGCTCTACATTTAGTTGGTGATCATATAATTTATATATTATCAT	1377		
DB	170	AGCACTGTATTGCTACACATTCATTTTGCCACTGTGATGATATGTTATCTCAATTGTGC	229		
QY	1378	ATAAATTGATCAACTTGGAGATGCTTTTGACTTCTCAAGATTTCTTGGAAATGACTTAT	1433		
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RESULT 15
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; Sequence 15974, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15974
; LENGTH: 294836
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(294836)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15974

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GenCore version 5.1.6
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(without alignments)
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Title: US-10-751-612-1

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
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- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
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- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
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- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
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- 21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	3016	100.0	3016	18	US-10-751-612-1	Sequence 1, Appli
2	120.8	4.0	576	18	US-10-425-115-151068	Sequence 151068, A
3	120.2	4.0	622	18	US-10-767-701-19690	Sequence 19690, A
4	118.6	3.9	3688	9	US-09-866-153-10	Sequence 10, Appl
5	118.6	3.9	3691	9	US-09-866-153-3	Sequence 3, Appli
6	118.6	3.9	5174	9	US-09-866-153-8	Sequence 8, Appli
7	100.8	3.3	1346	18	US-10-767-701-11451	Sequence 11451, A
8	96.4	3.2	398	18	US-10-767-701-18110	Sequence 18110, A
9	89.4	3.0	1318	18	US-10-767-701-10015	Sequence 10015, A
10	89.4	3.0	2032	18	US-10-425-115-42192	Sequence 42192, A
11	88	2.9	1894	17	US-10-425-114-32756	Sequence 32756, A

C	12	1894	2.9	1894	18	US-10-425-115-183742	Sequence 183742, A
	13	1285	2.9	1285	17	US-10-425-114-24208	Sequence 24208, A
	14	86.2	2.9	1360	18	US-10-425-115-142566	Sequence 142566, A
	15	86.2	2.9	1382	18	US-10-425-115-165368	Sequence 165368, A
	16	83.6	2.8	690	18	US-10-767-701-170788	Sequence 170788, A
	17	78.8	2.6	586	18	US-10-767-701-101717	Sequence 17017, Ap
	18	66.8	2.2	2000	17	US-10-425-115-133113	Sequence 1707, Ap
	19	66	2.2	129	18	US-10-425-115-133113	Sequence 133113, A
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	22	62.2	2.1	1663	18	US-10-425-115-25020	Sequence 25020, A
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	25	61.4	2.0	439	18	US-10-437-963-31959	Sequence 31959, A
	26	61.2	2.0	290	9	US-09-923-876-3721	Sequence 3721, Ap
	27	61.2	2.0	290	10	US-09-923-876-3721	Sequence 3721, Ap
	28	61.2	2.0	1374	17	US-10-425-114-3568	Sequence 3568, Ap
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	30	60.8	2.0	439	18	US-10-437-963-42140	Sequence 42140, A
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	33	60.6	2.0	1894	17	US-10-425-114-32756	Sequence 32756, A
	34	60.6	2.0	1894	18	US-10-425-115-183742	Sequence 183742, A
	35	59.8	2.0	1309	17	US-10-425-114-35130	Sequence 35130, A
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	37	59.2	2.0	255	18	US-10-437-963-62353	Sequence 62353, A
	38	58	1.9	326	18	US-10-437-963-93872	Sequence 93872, A
	39	57.8	1.9	442	18	US-10-437-963-66554	Sequence 66554, A
	40	57.6	1.9	305	18	US-10-437-963-95390	Sequence 95390, A
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	42	57.6	1.9	2000	17	US-10-437-963-2371	Sequence 2371, Ap
	43	57.4	1.9	442	18	US-10-437-963-42065	Sequence 42065, A
C	44	57.2	1.9	441	18	US-10-437-963-31961	Sequence 31961, A
	45	57	1.9	452	18	US-10-437-963-30623	Sequence 30623, A

ALIGNMENTS

RESULT 1

US-10-751-612-1
; Sequence 1, Application US/10751612
; Publication No. US2005005322A1
; GENERAL INFORMATION:
; APPLICANT: Mirkov, T. Erik
; APPLICANT: Damaj, Mona B.,
; APPLICANT: Reddy, Avutu,
; APPLICANT: Thomas, Terry L.,
; APPLICANT: Rathore, Keerti S.,
; APPLICANT: Emami, Chandrakanth,
; APPLICANT: Kumpatla, Siva Prasad
; TITLE OF INVENTION: STEM-REGULATED, PLANT DEFENSE PROMOTER
; FILE OF INVENTION: AND USES THEREOF IN TISSUE-SPECIFIC EXPRESSION IN MONOCOTS
; FILE REFERENCE: 017575.0774
; CURRENT APPLICATION NUMBER: US/10/751.612
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: 60/437,890
; PRIOR FILING DATE: 2003-01-03
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3016
; TYPE: DNA
; ORGANISM: Sugarcane
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)...(3012)
; OTHER INFORMATION: o-methyltransferase promoter
; FEATURE:
; NAME/KEY: CAAT signal
; LOCATION: (2661)...(2664)
; NAME/KEY: TATA_signal

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QY 2281 TTTTGGCTGCCAAGTGTGGAACAACCTCAAGGTAAAGTCCCACTCAATCTTAAATGATGTC 2340
Db 2281 TTTTGGCTGCCAAGTGTGGAACAACCTCAAGGTAAAGTCCCACTCAATCTTAAATGATGTC 2340
QY 2341 CAAATAAAGATAGATTACAAAGTTAAACGACGGAAGTCTTAAATAGGATGGAAGTT 2400
Db 2341 CAAATAAAGATAGATTACAAAGTTAAACGACGGAAGTCTTAAATAGGATGGAAGTT 2400
QY 2401 TTGTAGAGTAAATATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2460
Db 2401 TTGTAGAGTAAATATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2460
QY 2461 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2520
Db 2461 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2520
QY 2521 TTGCAATTTTGCACCCCTTAATGTTAATCAAGGTGCTCACTTAGGATGCTCACTCACTCACTCA 2580
Db 2521 TTGCAATTTTGCACCCCTTAATGTTAATCAAGGTGCTCACTTAGGATGCTCACTCACTCACTCA 2580
QY 2581 ATGCAATTTTGCATACCTAGTGTGTTCAAGGTGCTCACTTAGGATGCTCACTCACTCACTCACT 2640
Db 2581 ATGCAATTTTGCATACCTAGTGTGTTCAAGGTGCTCACTTAGGATGCTCACTCACTCACTCACT 2640
QY 2641 ATTTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2700
Db 2641 ATTTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2700
QY 2701 GATGACCCCAATATAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2760
Db 2701 GATGACCCCAATATAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2760
QY 2761 ATAATCTTTTCAAGTGTAGTACTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTT 2820
Db 2761 ATAATCTTTTCAAGTGTAGTACTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTT 2820
QY 2821 GAATTCGGAAGTACTATAAAGCGGAGCCTATAAATGGAGAGCTTTTTCATCATGATGAGCTA 2880
Db 2821 GAATTCGGAAGTACTATAAAGCGGAGCCTATAAATGGAGAGCTTTTTCATCATGATGAGCTA 2880
QY 2881 TAACAACCTTGAGCAAAAAACAGAAAGCGTCCGCTAGGCTCAGCAAGGAGCAACACACA 2940
Db 2881 TAACAACCTTGAGCAAAAAACAGAAAGCGTCCGCTAGGCTCAGCAAGGAGCAACACACA 2940
QY 2941 AGCACTGATCAGCAGCGCTGCTGATGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCT 3000
Db 2941 AGCACTGATCAGCAGCGCTGCTGATGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCT 3000
QY 3001 TATGTCAGAGTCCATCG 3016
Db 3001 TATGTCAGAGTCCATCG 3016
```

RESULT 2
US-10-425-115-151068
; Sequence 151068, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 151068
LENGTH: 576
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_69292C.1
US-10-425-115-151068

Query Match 4.0%; Score 120.8; DB 18; Length 576;
Best Local Similarity 66.9%; Pred. No. 5.5e-22;
Matches 198; Conservative 0; Mismatches 77; Indels 21; Gaps 1;

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QY 278 AGAATGTTGATCTGGAGAGTCTTCTGAGATGTGACAAACGCGGAGGTCTATATCAAGA 337
Db 281 AGAATGTTGATCTACATAGGTTCTATGAGGATGCGACAAACACAGAGGCTATATCAAGA 340
QY 338 TTCTGGGTACCCGGGAGAAATCGGCCTCCATGTAGTTAGCCTCGTCAGGCATGGGGGAA 397
Db 341 CTCTGGGTACATGAGGAGAAATCGTCTCCATGTGTTGCTCTCGTCAGGCATGGGGGAA 400
QY 398 TTGCTGAGATGCCCCCATGTA-----GTCTGAGGCATGGAGA 436
Db 401 TTGCTGAGATGCCCCCATGTAAGTCTGTTGGCACTGGTGTCTGTCAGGCATGGAGA 460
QY 437 GTACTGCTGAGATGCCCATTTGTTGTAGATCGAGAGAAACGAGAGAAATGCTAGTCTAA 496
Db 461 GAATGGGTGAGATGTGAGAGAAACGAGAGAAATGCTAAATACCTTCCGTAT 520
QY 497 TAATACCTTCCGTATGCTAAACCACTATTATAATTTGGCACCATTTCATCATGCT 552
Db 521 CTAGATGATATTTGATGGAACCACTATTATAATAGGCCATTTTTCACAGGCT 576
```

RESULT 3

US-10-767-701-19690
; Sequence 19690, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 19690
LENGTH: 622
TYPE: DNA
ORGANISM: Sorghum bicolor
FEATURE:
OTHER INFORMATION: Clone ID: LIB5047-010-R1-XP1-B5
US-10-767-701-19690

Query Match 4.0%; Score 120.2; DB 18; Length 622;
Best Local Similarity 66.7%; Pred. No. 8.4e-22;
Matches 198; Conservative 0; Mismatches 78; Indels 21; Gaps 1;

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QY 278 AGAATGTTGATCTGGAGAGTCTTCTGAGATGTGACAAACGCGGAGGTCTATATCAAGA 337
Db 304 AGAATGTTGATCTACATAGGTTCTATGAGGATGCGACAAACACAGAGGCTATATCAAGA 363
QY 338 TTCTGGGTACCCGGGAGAAATCGGCCTCCATGTAGTTAGCCTCGTCAGGCATGGGGGAA 397
```

Db 364 CTCCTGGTACATGAGGAGAACTGCTCTTCATGTGCTTTGCTCTCGTCAGGCATGGGGCAA 423
QY 398 TTGGCTGAGATGCCCCCATGTA-----GTCGTACGATGGAGA 436
Db 424 TTGGCTGAGATGCCCCCGTATAGCTGGTCTTTGTTGGCACTGGTGTGCTGAGGCATGGAGA 483
QY 437 GTACTGGCTGAGATGCCATTTGTTGTAGATCGAGAGAAACGAGAGAAGATGCTAGTCTAA 496
Db 484 GAAATTGGGTGAGATTGAGAGAAACGAGAGAAGATGCTAATCTAATTACCTTCCTGAT 543
QY 497 TAATACCTTCCTGATGCTAACCACTATTAATATGACCACTTTTACATGCTA 553
Db 544 CTAGATGATAATTGATGGAACCACTATTATAATTAGCGCATTTTTCACAGGCAA 600

RESULT 4

US-09-866-153-10/c
; Sequence 10, Application US/09866153
; Patent No. US2002004615A1
; GENERAL INFORMATION:
; APPLICANT: Albert, Henrik H.
; APPLICANT: Wei, Hairong
; TITLE OF INVENTION: PLANT PROMOTER SEQUENCES AND METHODS OF USE THEREOF
; FILE REFERENCE: UH-03648
; CURRENT APPLICATION NUMBER: US/09/866,153
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 09/270,976
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 3688
; TYPE: DNA
; ORGANISM: Saccharum Hybrid Cultivar 32-8560
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (9)
; OTHER INFORMATION: The "n" at position 9 is any nucleotide.
US-09-866-153-10

Query Match 3.9%; Score 118.6; DB 9; Length 3688;
Best Local Similarity 86.0%; Pred. No. 7.1e-21;
Matches 166; Conservative 0; Mismatches 24; Indels 3; Gaps 3;
QY 1451 AGTTTCTAAGCCAGTCTCAGTGGGGTTTCATCAGAGTTTCATGACATTAATAAGCT 1510
Db 1914 AGTTTCTGAGCCCGTCTCAGT-GGATTTTCATCAGAGTTTCATGACATTAATAAGCT 1856
QY 1511 GATGTGACACCGTATTGATGAAGAGAGATGATGAAGAGTTTCATGCGAGTAGAGAGAGT 1570
Db 1855 GATGTGGCACCGTATTGATGAAGAGAGATGATGAAGAGTTTCATGGAATTAGAGAGAGT 1796
QY 1571 TTTCATGGGATGAACACTCTT-CTTCACCTGTTTCCAAAATAT-AGATGCATTGGTAAGAGG 1628
Db 1795 TTTCAGGAAGATGAACACTCTCTCTGCACTGTTTCCAAAATATGGGTTCATTAAATAACATG 1736
QY 1629 GCCATGAATCTC 1641
Db 1735 GCCATAAAATCCC 1723

RESULT 5

US-09-866-153-3/c
; Sequence 3, Application US/09866153
; Patent No. US2002004615A1
; GENERAL INFORMATION:
; APPLICANT: Albert, Henrik H.
; APPLICANT: Wei, Hairong
; TITLE OF INVENTION: PLANT PROMOTER SEQUENCES AND METHODS OF USE THEREOF
; FILE REFERENCE: UH-03648
; CURRENT APPLICATION NUMBER: US/09/866,153
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 09/270,976

; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 3691
; TYPE: DNA
; ORGANISM: Saccharum Hybrid Cultivar H32-8560
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (9)
; OTHER INFORMATION: The "n" at position 9 is any nucleotide.
; NAME/KEY: misc_feature
; LOCATION: (3613)
; OTHER INFORMATION: The "n" at position 3613 is any nucleotide.
US-09-866-153-3

Query Match 3.9%; Score 118.6; DB 9; Length 3691;
Best Local Similarity 86.0%; Pred. No. 7.1e-21;
Matches 166; Conservative 0; Mismatches 24; Indels 3; Gaps 3;
QY 1451 AGTTTCTAAGCCAGTCTCAGTGGGGTTTCATCAGAGTTTCATGACATTAATAAGCT 1510
Db 1914 AGTTTCTGAGCCCGTCTCAGT-GGATTTTCATCAGAGTTTCATGACATTAATAAGCT 1856
QY 1511 GATGTGACACCGTATTGATGAAGAGAGATGATGAAGAGTTTCATGCGAGTAGAGAGAGT 1570
Db 1855 GATGTGGCACCGTATTGATGAAGAGAGATGATGAAGAGTTTCATGGAATTAGAGAGAGT 1796
QY 1571 TTTCATGGGATGAACACTCTT-CTTCACCTGTTTCCAAAATAT-AGATGCATTGGTAAGAGG 1628
Db 1795 TTTCAGGAAGATGAACACTCTCTCTGCACTGTTTCCAAAATATGGGTTCATTAAATAACATG 1736
QY 1629 GCCATGAATCTC 1641
Db 1735 GCCATAAAATCCC 1723

RESULT 6

US-09-866-153-8/c
; Sequence 8, Application US/09866153
; Patent No. US2002004615A1
; GENERAL INFORMATION:
; APPLICANT: Albert, Henrik H.
; APPLICANT: Wei, Hairong
; TITLE OF INVENTION: PLANT PROMOTER SEQUENCES AND METHODS OF USE THEREOF
; FILE REFERENCE: UH-03648
; CURRENT APPLICATION NUMBER: US/09/866,153
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 09/270,976
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 5174
; TYPE: DNA
; ORGANISM: Saccharum Hybrid Cultivar H32-8560
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (9)
; OTHER INFORMATION: The "n" at position 9 is any nucleotide.
; NAME/KEY: misc_feature
; LOCATION: (4318)
; OTHER INFORMATION: The "n" at position 4318 is any nucleotide.
; NAME/KEY: misc_feature
; LOCATION: (4546)
; OTHER INFORMATION: The "n" at position 4546 is any nucleotide.
; NAME/KEY: misc_feature
; LOCATION: (4890)
; OTHER INFORMATION: The "n" at position 4890 is any nucleotide.
; NAME/KEY: misc_feature
; LOCATION: (5117)
; OTHER INFORMATION: The "n" at position 5117 is any nucleotide.
; NAME/KEY: misc_feature

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; LOCATION: (5125)
; OTHER INFORMATION: The "n" at position 5125 is any nucleotide.
; NAME/KEY: misc feature
; LOCATION: (5150)
; OTHER INFORMATION: The "n" at position 5150 is any nucleotide.
US-09-866-153-8

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Query Match 3.9%; Score 118.6; DB 9; Length 5174;
Best Local Similarity 86.0%; Pred. No. 8.8e-21;
Matches 166; Conservative 0; Mismatches 24;
Indels 3; Gaps 3;

Qy	1451	AGGTTTCTAAGCCAGCTCTCAGTGGGGTTTCATCAGAGTTTCATGGA	1510
Db	1914	AGTTTTCTGAGGCCGCTCTCAGT-GGATTTTCATCAGAGTTTCATGGA	1856

Qy	1511	GATGTGACACCGTATTGATGTAAGAGAGAGATGATAAGAGTTCATCGGAGTAGAGAGAGT	1570
Db	1855	GATGTGGACCGTATTGATGTAAGAGAGAGAGATGATAAGAGTTCATGTGAATTTAGAGAGAGT	1796

Qy	1571	1795	1736
Db	TTCATGGGATGAAACTCTT - CTTCACTGTTTCCAAATAT - AGATGCATTGTTAAGAGG	TTTACGAAGATGAAACTCTTCTGCACCTGTTTCCAAATATGGTTCATTATTAACATG	

Qy 1629 GCCATGAAATCTC 1641
Db 1735 GCCATAAAATCCC 1723

RESULT 7
US-10-767-701-11451/c
; Sequence 11451, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yinhua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701

; CURRENT FILING DATE: 2004-01-29
 ; NUMBER OF SEQ ID NOS: 63128

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; NUMBER OF SEQ
; SEQ ID NO 11451
; LENGTH: 1346

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LENGTH: 1340
TYPE: DNA

ORGANISM:
FEATURE:

OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS3954_1
US-10-767-701-11451

Query Match 3.3%; Score 100.8; DB 18; Length 1346;
Best Local Similarity 70.2%; Pred. No. 2.9e-16;
Matches 160; Conservative 0; Mismatches 47; Indels 21; Gaps 1

Qy	1455	TTCTAAGCCGAGTCTCAGTGGGTTTCATCAGAGTTTCATGGACATTAAATAAGCTGATG	1514
Dβ	1291	TACTAAGCCGAGCTCAATGGAGTTTCATGAGAGTTTCATGCACATTAAATGCTGTGATG	1332

Qy	1515	TGACACCGTATTGATGATGAAGAGAGAGATGATGAATAGAGTTCCTCATGCGAGTAGAGAGAGAGTTC	1574
Dβ	1231	TGCGCGCTATAGTAAATGAAGAGAGAGATCATAGAGTTTTATCC	1189

QY 1575 TGGGGATGAAACTCTTCTTCACTGTTTCCAAATATAGATGCATTGTTGAAGAGGGCCATG 1634
1188 ----CATGAAACTTAAGGCATGTTTCCAAATACAGATGCTGTGAAATCATGGGCTATG 1133
Db

. Qr .

1635	AAATCTCTAGTGTACACATGACCTTATGATGAGATTCATCTAGCACATATG	1688
1122	AAATCTCTAGTGTACACATGACCTTATGATGAGATTCATCTAGCACATATG	1095
1123	AAATCTCTAGTGTACACATGACCTTATGATGAGATTCATCTAGCACATATG	1096

RESULT 8
US-10-767-701-18110/c

```

; Sequence 18110, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecule
; TITLE OF INVENTION: Plants and Uses Thereof
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 18110
; LENGTH: 398
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; US-10-767701-18110
; OTHER INFORMATION: Clone ID: LIB34478-007
; US-10-767701-18110

```

Query Match 3.2%; Score 96.4; DB 18; Length 398;
Best Local Similarity 79.4%; Pred. No. 2.1e-15;
Matches 127; Conservative 0; Mismatches 31; Indels 2; Gaps 1;

QY 1449 GPAGGTTTCTAAGCCCAAGTCTCAGTGGGGTTTTCATCAGAGTTTTCATCGACATTAAATAAG 1508

DP 158 GGAGGCCATACAAGTGTCTCTGTTAGGCCACTCTCAATGGAGTTTTCATTAAACATTAAATATG 99

QY 1509 CTGATGTGACACCGTATTGATGAAGAGAGAGATGATTAAGAGTTTCATCGGAGTAGAGAGA 1568

DP 98 CTGA--TGCCACCGTATTAAAGAGAGAGAGATGATTAAGAGTTTCATCGAAGTAGAGAGA 41

1569 GTTTCATGGGGATGAAACCTCTCTCTTCACTGTGTTCCAAAT 1608

1569 GTTTCATGGGGAATGATACCTCTCTCTCACAGTCTCCATTA
 |||||
 40 GTTTTATGGGGATGAAACTCTCTCTGCACTATTTTCCAAAT

RESULT 9

US-10-767-701-10015
; Sequence 10015, Application US/10767701

Publication No. US20040172684A1
GENERAL INFORMATION:

APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701

; CURRENT FILING DATE: 2004-01-29

; NUMBER OF SEQ ID NOS: 63128

; SEQ ID NO 1001

```

; LENGTH: 1318
; TYPE: DNA

```

ORGANISM: Sorghum bicolor

FEATURE:
OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS4887_1

Query Match 3.0%; Score 89.4; DB 18; Length 1318;
Best Local Similarity 80.2%; Pred. No. 3.8e-13;
Matches 105; Conservative 0; Mismatches 26; Indels 0;

	1456	TCTAAGCCCGTCTCAGTGGGTTTCATCAGAGTTTCATGGACATTAAATAAGCTGATGT	1515
b ₉			
Dh	1188	TCTTAGACCGGTCATGGAGTTTCATTAATTTTCATGCACATTAAATATGTGTTAAATGT	1247

Qy	1516	GACACCGTATTGATGAAGAGAGAGATGATAAGAGTTTCATGCGAGTAGAGAGAGATTTCAT	1575
Dh	1248	TGCTATGCTATTTAATGACAGAGAGAGATGATGATACAGGTTTCATGCAAGCAGACAGAGAGTTTAT	1307

QY 1576 GGGGATGAAAC 1586

Db 1308 CATCAAAAC 1318

RESULT 10

US-10-425-115-42192
; Sequence 42192, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 42192
; LENGTH: 2032
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_138478C.1
US-10-425-115-42192

Query Match 3.0%; Score 89.4; DB 18; Length 2032;

Best Local Similarity 68.9%; Pred. No. 5e-13;
Matches 151; Conservative 0; Mismatches 66; Indels 2; Gaps 2;

QY 1457 CTAAGGCCAGTCTCAGTGG-GGTTTCATCAGAGTTCATGGACATTAAATAAGCTGATGT 1515
DB 498 CTAAGACTAGTCTCTGTGTGTGTTTCACGAGGATTATGGCATTAATATGTTGATGT 557
QY 1516 GACACCGTATTGATGAAGAGAGAGATGATAAGAGTTTTCATGCGAGPAGAGAGTTTCAT 1575
DB 558 GGCATATTATTAAACGAAGAGAGATAAGGTAAAAAGTTTTATCGAATGAATGAGTTCCAC 617
QY 1576 GGG-GATGAACCTTTCTTCACCTGTTCCAAATATAGATGATGATGTTGAAGGGCCCATG 1634
DB 618 GGCGCATGAACCTTATGTGACCTGCTTCTAACAATATCGAGTCTTGGGAACATTGACATA 677
QY 1635 AAATCTCTAGTGCACCTGACCTTAAGATGAGATTGACTCT 1673
DB 678 AAATCCCACTGAACTGGCCCTAAATAAAGCTAATCT 716

RESULT 11

US-10-425-114-32756/c
; Sequence 32756, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 32756
; LENGTH: 1894
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-2MFLM017052G10_FLI
US-10-425-114-32756

Query Match 2.9%; Score 88; DB 17; Length 1894;

Best Local Similarity 83.3%; Pred. No. 1.2e-12;
Matches 100; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 2452 AAAGAGTTAAATGCATGATGATGCTCTTGAATCTTCTGGAGGTGCCACTTAGGTCCCAA 2511
DB 666 AAAGAGTTAAATGCATGATGATGCTCTTGAATCTTCTGGAGGTGCCACTTAGGTCCCAA 607
QY 2512 ACTCTCAAAATGCAATTTTGACACCCCTAAATGTTTCAAGTGTGCCACTTAGATCTACAA 2571
DB 606 ACTCTCAAAATGCAATTTTTGGCACCCCTAAATGTTTCAAGTGTGTCTACTTAGGTCCCAA 547

RESULT 12

US-10-425-115-183742/c
; Sequence 183742, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 183742
; LENGTH: 1894
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_99156C.1
US-10-425-115-183742

Query Match 2.9%; Score 88; DB 18; Length 1894;

Best Local Similarity 83.3%; Pred. No. 1.2e-12;
Matches 100; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 2452 AAAGAGTTAAATGCATGATGATGCTCTTGAATCTTCTGGAGGTGCCACTTAGGTCCCAA 2511
DB 666 AAAGAGTTAAATGCATGATGATGCTCTTGAATCTTCTGGAGGTGCCACTTAGGTCCCAA 607
QY 2512 ACTCTCAAAATGCAATTTTGACACCCCTAAATGTTTCAAGTGTGCCACTTAGATCTACAA 2571
DB 606 ACTCTCAAAATGCAATTTTTGGCACCCCTAAATGTTTCAAGTGTGTCTACTTAGGTCCCAA 547

RESULT 13

US-10-425-114-24208
; Sequence 24208, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 24208
; LENGTH: 1285
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3608-006-C5_FLI
US-10-425-114-24208

Query Match 2.9%; Score 86.2; DB 17; Length 1285;
Best Local Similarity 81.3%; Pred. No. 2.9e-12;
Matches 100; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 2894 AAAACAGAGCCGTGGCGCATGGCGCTCAGCAAGAGGAGCAACACAAAGCACTGATCAGC 2953
DB 41 AAAAGCACGAGCTCAGCGCATGGCGCCGCGCAAAAGCGCAGCACACAAAGCACTAACCCAGC 100

QY 2954 AGGCGGTGCTGGATGCTCAGCTCCAGCTCTGGCACCACACACCTGGGCTATGTCAAGTCCA 3013
DB 101 AGACATTGCTGGATGGCGAGCTCCAGCTCTGGCATCACGCTTCGGCTACGTCAAGTCCA 160

QY 3014 TGG 3016
DB 161 TGG 163

RESULT 14
US-10-425-115-142566
; Sequence 142566, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 142566
; LENGTH: 1360
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_61502C.1
US-10-425-115-142566

Query Match 2.9%; Score 86.2; DB 18; Length 1360;
Best Local Similarity 81.3%; Pred. No. 2.9e-12;
Matches 100; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 2894 AAAACAGAGCCGTGGCGCATGGCGCTCAGCAAGAGGAGCAACACAAAGCACTGATCAGC 2953
DB 79 AAAGCACGAGCTCAGCGCATGGCGCCGCGCAAAAGCGCAGCACACAAAGCACTAACCCAGC 138

QY 2954 AGGCGGTGCTGGATGCTCAGCTCCAGCTCTGGCACCACACACCTGGGCTATGTCAAGTCCA 3013
DB 139 AGACATTGCTGGATGGCGAGCTCCAGCTCTGGCATCACGCTTCGGCTACGTCAAGTCCA 198

QY 3014 TGG 3016
DB 199 TGG 201

RESULT 15
US-10-425-115-165368
; Sequence 165368, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 165368

; LENGTH: 1382
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_82401C.1
US-10-425-115-165368

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Best Local Similarity 87.9%; Pred. No. 2.9e-12;
Matches 94; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 2910 CGCATGGCGCTCAGCAAGAGGAGCAACACAAAGCACTGATCAGCAGGCCGTGCTGGATGC 2969
DB 14 CGCCATGACGCTCAGCAAGAGGAGGCGCAGGCACTGATCAGCAGGCCCTTGTGGATGC 73

QY 2970 TCAGCTCCAGCTCTGGCACCACACCTGGGCTATGTCAAGTCCATGG 3016
DB 74 TCAGCTGCAGCTCTGGCACCACACCATCGCTTTGTCAAGTCCATGG 120

Search completed: February 16, 2005, 11:04:46
Job time : 1985 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 15, 2005, 22:03:37 ; Search time 9452 Seconds
(without alignments)
12145.772 Million cell updates/sec

Title: US-10-751-612-1

Perfect score: 3016

Sequence: 1 tctagagcataggcatgtga.....gggctatgtcaagtcctatgg 3016

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_hcc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gse1:*
9: gb_gse2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	320.4	10.6	322	6	CA113147	CA113147 SCEZLB100
2	275.2	9.1	583	6	CA118968	CA118968 SCBGLR111
3	254.6	8.4	556	6	CA248733	CA248733 SCBFL110
4	164.6	5.5	674	6	CA203163	CA203163 SCRFLL102
5	161.6	5.4	563	6	CA128031	CA128031 SCAGLR201
6	158	5.2	664	6	CA154373	CA154373 SCVPRZ204
7	157.8	5.2	694	6	CA126310	CA126310 SCBGLR104
8	154.4	5.1	573	6	CA118511	CA118511 SCBGLR109
9	152.2	5.0	634	9	CW512557	CW512557 115_1_105
10	149.2	4.9	400	6	CA186194	CA186194 SCBGLR111
11	148.6	4.9	717	9	CL192172	CL192172 104_414_1
12	147.8	4.9	669	6	CA220522	CA220522 SCRFL402
13	147.4	4.9	740	9	CL191874	CL191874 104_414_1
14	141.8	4.7	1273	8	BZ693362	BZ693362 SP_Ba003
15	139.4	4.6	787	8	BZ342445	BZ342445 ic8e09.g
16	136.2	4.5	732	8	BZ715359	BZ715359 PUFAD81TD
17	136.2	4.5	907	9	CG369374	CG369374 OG0GR27TV
18	136.2	4.5	921	9	CG068037	CG068037 PU1IC82TB
19	133.8	4.4	591	8	BZ692106	BZ692106 SP_Ba001
20	130.6	4.3	664	8	BZ692043	BZ692043 SP_Ba001
21	129	4.3	680	8	BZ626898	BZ626898 ih49a06.b
22	128.8	4.3	623	9	CL193585	CL193585 104_417_1
23	126.6	4.2	631	9	CW512200	CW512200 115_1_105
24	126.4	4.2	708	8	BZ343488	BZ343488 ho55h06.b

25	126.2	4.2	734	6	CF070857	CF070857 FEL_14_B0
26	125.2	4.2	622	8	BZ629605	BZ629605 ih67c10.b
27	123.6	4.1	624	6	CA186182	CA186182 SCGST311
28	122.8	4.1	559	6	CA118575	CA118575 SCBGLR110
29	120.8	4.0	419	9	CL1701972	CL1701972 SP_Ba007
30	120.8	4.0	747	9	CL152042	CL152042 104_335_1
31	119.6	4.0	1246	8	BZ694416	BZ694416 SP_Ba004
32	118.6	3.9	925	9	CG295925	CG295925 OG0FA16TV
33	115.6	3.8	334	8	BZ629606	BZ629606 ih67c10.g
34	115.6	3.8	389	8	BZ989929	BZ989929 PUDFG82TD
35	114.2	3.8	512	5	BQ536419	BQ536419 STEM4_A
36	114.2	3.8	513	5	BQ536474	BQ536474 STEM4_1_D
37	114.2	3.8	625	5	BQ537299	BQ537299 STEM2_23
38	114.2	3.8	637	5	BQ536451	BQ536451 STEM4_1_B
39	113.8	3.8	770	9	CL167477	CL167477 104_364_1
40	113.8	3.8	782	9	CL167479	CL167479 104_364_1
41	113.4	3.8	726	9	CL154621	CL154621 104_340_1
42	113	3.7	630	8	CC059054	CC059054 1118f07.b
43	111.2	3.7	637	6	CA195175	CA195175 SCEZSB109
44	111.2	3.7	660	5	BQ536496	BQ536496 STEM4_1_E
45	110.8	3.7	658	6	CA210698	CA210698 SCEPSB113

ALIGNMENTS

RESULT 1
CA113147
LOCUS SCEZLB1009D09.g LB1 Saccharum officinarum cdna clone SCEZLB1009D09
DEFINITION 322 bp mRNA linear EST 23-SEP-2003
5', mRNA sequence.
ACCESSION CA113147
VERSION CA113147.1 GI:34966454
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
complex.
REFERENCE 1 (bases 1 to 322)
AUTHORS Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
TITLE The libraries that made SUCEST
JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 009 row: D column: 09
Seq primer: T7 Promoter Primer.
Location/Qualifiers
1. 322
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCEZLB1009D09"
/lab_host="DH10B"
/clone_lib="LB1"

note="Organ: Lateral buds from field grown adult plants;
Vector: pSport1; Site 1: SalI; Site 2: NotI; An
unidirectional cDNA library generated from [lateral buds
from field grown adult plants]. cDNA was prepared from
polyA+ mRNA using SuperScript Plasmid System kit
(Invitrogen). The double-strand cDNAs were fractionated
in a spherose CL-2B 40cm-columns and fragments sizing
between 0.8 and 1.5 kb were directionally cloned into the
vector. Details of each source of RNA and library

/clone_lib="Fli1"
 /note="Organ: Inflorescence at beginning of development (lcm-long); Vector: pSport1; Site_1: SalI; Site_2: NotI; An unidirectional cDNA library generated from [Inflorescence at beginning of development (lcm-long)]. cDNA was prepared from polyA+ mRNA using Superscript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucust.lad.ic.unicamp.br/public"

ORIGIN

Query Match 8.4%; Score 254.6; DB 6; Length 556;
 Best Local Similarity 97.5%; Pred. No. 5.5e-58;
 Matches 270; Conservative 0; Mismatches 4; Indels 3; Gaps 1;
 QY 272 AGATGAAGAATGTCATCTGGAGAAGTTTGTGAGAATGTGACAAACGGGAGGTCTATA 331
 Db |||||
 QY 277 AGATGAAGAATGTCATCTGGAGAAGTTTGTGAGAATGTGACAAACAGGAGGTCTATA 218
 Db |||||
 QY 332 TCAAGATTCTGGTACCGCGAGAAATCGGCTCCATGTAGTTAGCTTCGTCAGGCATGG 391
 Db |||||
 QY 217 TCAAGATTCTGGTACCGCGAGAAATCGGCTCCATGTAGTTAGCTTCGTCAGGCATGG 158
 Db |||||
 QY 392 GGGGAATTGGCTGAGATGCCCCATGTAGTCTCAGGCATGGAGAGTACTGCTCAGATG 451
 Db |||||
 QY 157 GGGGAATTGGCTGAGATGCCCCATGTAGTCTCAGGCATGGAGAGTACTGCTCAGATG 98
 Db |||||
 QY 452 CCATTGTTGTGTAGATCGAGAGAAACGAGAGAATGCTAGTCTAATAATACCCCTTCCGTA 511
 Db |||||
 QY 97 CCATTGTTGTGTAGATCGAGAGAAACGAGAGAATGCTAGTCTAATAATAGTACCCCTTCCGTA 38
 Db |||||
 QY 512 TG---CTAACCACTATTATTAATGGCCACATTTTC 545
 Db |||||
 QY 37 TGATCTAACCACTATTATTAATGGCCACATTTTC 1

RESULT 4

CA203163
 LOCUS SCRFLL1028D06.g Fli1 Saccharum officinarum cDNA clone SCRFLL1028D06
 DEFINITION 5', mRNA sequence.
 ACCESSION CA203163
 VERSION CA203163.1 GI:35239153
 KEYWORDS EST.
 SOURCE Saccharum officinarum

ORGANISM

Saccharum officinarum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
 complex.

REFERENCE

1 (bases 1 to 674)
 Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
 The libraries that made SUCST

AUTHORS

Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
 Contact: Arruda P

JOURNAL

Centro de Biologia Molecular e Engenharia Genetica
 Universidade Estadual de Campinas
 Caixa Postal 6010, 13083-970, Campinas SP, Brazil
 Tel: 55 19 3788 1137
 Fax: 55 19 3788 1089

COMMENT

Email: parruda@unicamp.br
 Clone distribution: clone distribution information can be found
 through the Brazilian Clone Collection Center (BCCC) at:
 http://www.bcccenter.fcav.unesp.br

Plate:

028 row: D column: 06

Seq primer:

T7 Promoter Primer.

FEATURES

source

1..674

/organism="Saccharum officinarum"

/mol_type="mRNA"

/db_xref="taxon:4547"
 /clone="SCRFLL1028D06"
 /lab_host="DH10B"
 /clone_lib="Fli1"

/note="Organ: Inflorescence at beginning of development (lcm-long); Vector: pSport1; Site_1: SalI; Site_2: NotI; An unidirectional cDNA library generated from [Inflorescence at beginning of development (lcm-long)]. cDNA was prepared from polyA+ mRNA using Superscript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucust.lad.ic.unicamp.br/public"

ORIGIN

Query Match 5.5%; Score 164.6; DB 6; Length 674;
 Best Local Similarity 84.5%; Pred. No. 2.7e-33;
 Matches 185; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
 QY 1453 GTTCTAAGGCCAGTCTCAGTGGGGTTTCATCAGAGTTTCATGGACATTAATAGCTGA 1512
 Db |||||
 QY 258 GTGCTAAGGCCAGTCTCAGTGGGGTTTCATCAGAGTTTCATGGACATTAATAGCTGA 199
 Db |||||
 QY 1513 TGTGACACCGTATTGATGAAGAGAGAGATGATAGAGTTTCATGCGAGTAGAGAGTTT 1572
 Db |||||
 QY 198 TGTAGCACTATTATTATGAAGAGAGAGATGATAGAGTTTCATGCGAGTAGAGAGTTT 139
 Db |||||
 QY 1573 CATGGGATGAACCTCTTCTTCTCAGTCTTCCAAATATAGATGCTTGGTAAGAGGGCCA 1632
 Db |||||
 QY 138 CATGGAGATAAACCTCTTTTGCACCTGTTTCCAAATTTGGATGCGCTGGAAACAGTGACA 79
 Db |||||
 QY 1633 TGAATCTCTAGTACACTGACCTGACCTAAGATGATGACT 1671
 Db |||||
 QY 78 TGAATCTCTCATTGAGACTGGCTTAAGAGCAGGTACAGT 40
 Db |||||

RESULT 5

CA128031
 LOCUS SCAGLR2018H12.g LR2 Saccharum officinarum cDNA clone SCAGLR2018H12
 DEFINITION 5', mRNA sequence.

ACCESSION

CA128031

VERSION

CA128031.1

KEYWORDS

EST.

SOURCE

Saccharum officinarum
 Saccharum officinarum

ORGANISM

Saccharum officinarum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
 complex.

REFERENCE

1 (bases 1 to 563)
 Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
 The libraries that made SUCST

AUTHORS

Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
 Contact: Arruda P

JOURNAL

Centro de Biologia Molecular e Engenharia Genetica
 Universidade Estadual de Campinas
 Caixa Postal 6010, 13083-970, Campinas SP, Brazil
 Tel: 55 19 3788 1137
 Fax: 55 19 3788 1089

COMMENT

Email: parruda@unicamp.br
 Clone distribution: clone distribution information can be found
 through the Brazilian Clone Collection Center (BCCC) at:
 http://www.bcccenter.fcav.unesp.br

Plate:

018 row: H column: 12

Seq primer:

T7 Promoter Primer.

FEATURES

source

1..563

/organism="Saccharum officinarum"

/mol_type="mRNA"

/db_xref="taxon:4547"

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/clone="SCAGLR2018H12"
/lab_host="DH10B"
/clone_lib="LR2"
/notes="Organ: Leaf roll from field grown adult plants
(small insert library); Vector: pSport1; Site 1: SalI;
Site 2: NotI; An unidirectional cDNA library generated
from [leaf roll from field grown adult plants (small
insert library)]. cDNA was prepared from polyA+ mRNA
using Superscript Plasmid System Kit (Invitrogen). The
double-strand cDNAs were fractionated in a sepharose
CL-2B 40cm-columns and fragments sizing between 0.8 and
1.5 Kb were directionally cloned into the vector. Details
of each source of RNA and library construction can be
obtained at http://sucsest.lad.ic.unicamp.br/public"

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ORIGIN

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Query Match      5.4%; Score 161.6; DB 6; Length 563;
Best Local Similarity 82.0%; Pred. No. 1.7e-32;
Matches 200; Conservative 0; Mismatches 39; Indels 5; Gaps 1;

QY 277 AGAATGTTGACTGAGAGAGTTTGTGAGATGTGACAAACGGGAGGTCAATATCAAG 336
Db 318 AGGAATGTTGACTGAGAGAGTTTGTGAGATGTGACAAACGGGAGGTCAATATCAAG 377
QY 337 ATTCTGGGTACCGCGGAGATCGGCTCCATGTAGTTCGTCAGGCGATGGGGGA 396
Db 378 ATTCTGGGTACCGCGGAGATCGGCTTCATGTAGTTCGTCAGGCGATGGGGGA 437
QY 397 ATTGGCTGAGATGCCCCCA-----TGTAGTCTGAGGCGATGGAGATCTGGCTGAGATG 451
Db 438 AATTGCTGAGATGCCCCCGAGGAGTGCATCGTCAGGCGATGGAGAGATTGCTGAGATT 497
QY 452 CCATTGCTGTGATGCGAGAGAAACGAGAAAGTCTAGTCTAATATACCCCTCCGTA 511
Db 498 CCATTGTTGGTAGATTGGGAAACAAAGAAAGTCCCTGTCTAAATAATACCCCTTCGGAT 557
QY 512 TGCT 515
Db 558 TCCT 561

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RESULT 6

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CAL154373
LOCUS SCVPRZ2042F06.g R22 Saccharum officinarum cDNA clone SCVPRZ2042F06
DEFINITION 664 bp mRNA linear EST 24-SEP-2003
5', mRNA sequence.
ACCESSION CAL154373
VERSION CAL154373.1 GI:35061389
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
complex.

```

REFERENCE

```

1 (bases 1 to 664)
Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.
The libraries that made SUCSEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
Centro de Biologia Molecular e Engenhariaia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 042 row: F column: 06
Seq primer: T7 Promoter Primer.
Location/Qualifiers
1. .664

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FEATURES

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1. .664
/organism="Saccharum officinarum"

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/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCVPRZ2042F06"
/lab_host="DH10B"
/clone_lib="R22"
/notes="Organ: Shoot-root transition zone from young plants
(small insert library); Vector: pSport1; Site 1: SalI;
Site 2: NotI; An unidirectional cDNA library generated
from [shoot-root transition zone from young plants (small
insert library)]. cDNA was prepared from polyA+ mRNA
using Superscript Plasmid System Kit (Invitrogen). The
double-strand cDNAs were fractionated in a sepharose
CL-2B 40cm-columns and fragments sizing between 0.8 and
1.5 Kb were directionally cloned into the vector. Details
of each source of RNA and library construction can be
obtained at http://sucsest.lad.ic.unicamp.br/public"

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ORIGIN

```

Query Match      5.2%; Score 158; DB 6; Length 664;
Best Local Similarity 79.0%; Pred. No. 1.7e-31;
Matches 188; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1436 TTGGGGTAGGAGTAGGTTCTTAAGGCCAGTCTCAGTGGGGTTTCATCAGAGTTTCATG 1495
Db 159 TGTGTGCACAGTATGTTGTTAGTCACTCTAATGGGGTTTGATCAGAGTTTCATG 218
QY 1496 GACATTAAATAGCTGATGTGACACCGTATTGATGAAGAGAGATGATGAAGTTTCAT 1555
Db 219 GGCATTAAATATTGTTGATGTGACACCATTAATGAAGAGAGATGATGAAGTTTCAT 278
QY 1556 GCGAGTAGAGAGATTTTCATGGGATGAACTCTTCTCACTGTTCCAAATATAGATG 1615
Db 279 GGGAGTAGAGAGATTTTCATGAGATGAGACTCTTATGCACTGTTTCCAAATCTGGATG 338
QY 1616 CATTGTGAAGAGGGCCATGAATCTCTAGTGACACTGACCTTAAGATGAGATTGACTCT 1673
Db 339 TGTTGAAACAGTATGATGAATCCCACTGAACCTGCCCTTATGCGATGTTTCTTT 396

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RESULT 7

```

CAL126310/c
LOCUS SCVGLR1045G12.g LR1 Saccharum officinarum cDNA clone SCVGLR1045G12
DEFINITION 694 bp mRNA linear EST 24-SEP-2003
5', mRNA sequence.
ACCESSION CAL126310
VERSION CAL126310.1 GI:35005077
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
complex.

```

REFERENCE

```

1 (bases 1 to 694)
Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.
The libraries that made SUCSEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
Centro de Biologia Molecular e Engenhariaia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 045 row: G column: 12
Seq primer: T7 Promoter Primer.
Location/Qualifiers
1. .694
/organism="Saccharum officinarum"

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FEATURES

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source
1. .694
/organism="Saccharum officinarum"

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/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCSGLR1045G12"
/lab_host="DH10B"
/clone_lib="LRI"
/note="Organ: Leaf roll from field grown adult plants
(large insert library); Vector: pSport1; Site_1: SalI;
Site_2: NotI; An unidirectional cDNA library generated
from [Leaf roll from field grown adult plants (large
insert library)]. cDNA was prepared from polyA+ mRNA
using SuperScript Plasmid System Kit (Invitrogen). The
double-strand cDNAs were fractionated in a sepharose
CL-2B 40cm-columns and fragments sizing between 0.8 and
1.5 Kb were directionally cloned into the vector. Details
of each source of RNA and library construction can be
obtained at http://sucet.lad.ic.unicamp.br/public"

```

ORIGIN

```

Query Match      5.2%; Score 157.8; DB 6; Length 694;
Best Local Similarity 81.3%; Pred. No. 2e-31;
Matches 183; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 1451 AGTTTCTAAGCCAGTCTCAGTGGGTTTCATCAGAGTTTCATCGACATTAATAAGCT 1510
DB 373 AGTTTCTAAGCCAGTCTCAGTGGGTTTCATCAGAGTTTCATCGACATTAATAAGCT 314

QY 1511 GATGTGACACCGTATTGATGAAGAGAGATGATGAAGAGTTTCATGCGAGTAGAGAGT 1570
DB 313 AATGTGGCACCGTATTGATGAAGAGAGATGATGAAGAGTTTCATGCGAGTAGAGATCGT 254

QY 1571 TTCATGGGGATGAACACTCTTCTTCACTGTTTCCAAATATAGATGATCGTAAAGAGGCG 1630
DB 253 TTCATGGAGATGAACACTCTTCTGCACTGTTTCCAAATATAGATGCGTTGAACACTAGA 194

QY 1631 CATGAATCTCTAGTGACACGACCTAAGATGAGATGACTCTAG 1675
DB 193 CATGAATCTCAACTGAACTGGCCCTAAAGCAGTTGGCAACTG 149

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RESULT 8

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CAL18511
LOCUS      573 bp mRNA linear EST 23-SEP-2003
DEFINITION SCSGLR1099C01.g LRI Saccharum officinarum cDNA clone SCSGLR1099C01
5', mRNA sequence.
ACCESSION CAL18511
VERSION CAL18511.1 GI:34971819
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
complex.
REFERENCE 1 (bases 1 to 573)
AUTHORS Vettore,A.L., da Silva,P.R., Kemper,E.L. and Arruda,P.
TITLE The libraries that made SUCST
JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT Contact: Arruda P
Centro de Biologia Molecular e Engenhariaia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br

```

Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at <http://www.bcccenter.fcav.unesp.br>

Plate: 099 row: C column: 01
Seq primer: T7 Promoter Primer.

FEATURES

```

source
1..573
/organism="Saccharum officinarum"
/mol_type="mRNA"

```

```

/db_xref="taxon:4547"
/clone="SCBGLR1099C01"
/lab_host="DH10B"
/clone_lib="LRI"
/note="Organ: Leaf roll from field grown adult plants
(large insert library); Vector: pSport1; Site_1: SalI;
Site_2: NotI; An unidirectional cDNA library generated
from [Leaf roll from field grown adult plants (large
insert library)]. cDNA was prepared from polyA+ mRNA
using SuperScript Plasmid System Kit (Invitrogen). The
double-strand cDNAs were fractionated in a sepharose
CL-2B 40cm-columns and fragments sizing between 0.8 and
1.5 Kb were directionally cloned into the vector. Details
of each source of RNA and library construction can be
obtained at http://sucet.lad.ic.unicamp.br/public"

```

ORIGIN

```

Query Match      5.1%; Score 154.4; DB 6; Length 573;
Best Local Similarity 93.6%; Pred. No. 1.6e-30;
Matches 161; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 TCTAGACATAGGATTTGTAAGGGGTATGCTTCTTCTCAGTGCAGAAATTCATACCA 60
DB 402 TCTAGACATAGGATTTGTAAGGGGTATGCTTCTTCTCAGTGCAGAAATTCATACCA 461

QY 61 ACCTTAGGTATCTGTCTTCCATAGAATTTTCTACCTGAGTAGGTTCCGTTCTGGTTGGAT 120
DB 462 ACCTTAGGTATCTGTCTTCCATAGAATTTTCTACCTGAGTAGGTTCCGTTCTGGTTGGGA 521

QY 121 TTGTAGCGGGTTTCATGCAAAATAGTTAGAAATCGTGCAAACTTGCAATGG 172
DB 522 TTGTAGCGGGTTTCATGCAAAATAGTTAGAAATCGTGCAAACTTGCAATGG 573

```

RESULT 9

```

CW512557/c
LOCUS      634 bp DNA linear GSS 07-OCT-2004
DEFINITION 115.1.10510675.1 30023 sorghum unfiltered library (LibID: 115)
Sorghum bicolor genomic clone 10510675, genomic survey sequence.
ACCESSION CW512557
VERSION CW512557.1 GI:53855339
KEYWORDS GSS.
SOURCE Sorghum bicolor (sorghum)
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE 1 (bases 1 to 634)
AUTHORS Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
McMenamy,J., Smith,M., Holuman,H., Roe,B.A., Wiley,G., Korf,I.F.,
Rabinowitz,P.D., Lakey,N., McCombie,W.R., Jeddellon,J.A. and
Martienssen,R.A.
TITLE Sorghum genome sequencing by methylation filtration
JOURNAL Unpublished (2004)
COMMENT Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 1 row: P column: 17
Seq primer: M13(40)Forward
Class: shotgun
High quality sequence stop: 634.
Location/Qualifiers
1..634
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="Atx623"
/db_xref="taxon:4558"
/clone="10510675"
/clone_lib="Sorghum unfiltered library (LibID: 115)"

```

FEATURES

```

source
1..634
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="Atx623"
/db_xref="taxon:4558"
/clone="10510675"
/clone_lib="Sorghum unfiltered library (LibID: 115)"

```


prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBCSK(-) vector and electroporated into *E. coli* cells. This is a methylation-filtered library."

ORIGIN

```

Query Match      4.9%; Score 148.6; DB 9; Length 717;
Best Local Similarity 79.9%; Pred. No. 6.7e-29;
Matches 175; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 1454 TTCTAAGCCAGTCTCAGTGGGGTTTCATCAGAGTTTCATGGAATTAAATAAGCTGAT 1513
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 123 TFCATAAGACCAAGTCTCAATGGGGTTTCATTAGAGTTTCATGCACATTAATATCTGAT 182

QY 1514 GTGACACCGTATTGATGAAGAGAGAGATCATAGAGTTTCATGCCAGTAGAGAGTTTC 1573
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 183 GTGGCGCTATATTAATGAAGAGAGAGATGATAGAGTTTCATGGGAGTAGAGAGTTTC 242

QY 1574 ATGGGGATGAACCTCTTCTTCACTGTTTCCAAAATATAGATGCATTTGGTAAAGAGGCCAT 1633
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 243 ATCCCATGAACCTCTATGCACTGTTTCCAAAATATTGATGTGTTGGAACTGTGTAT 302

QY 1634 GAAATCTCTAGTGCACCTGACCTAAGATGAGATTGACTC 1672
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 303 GAAACTCCGTTGAGGAGTGCCCTAAGAGTAGAGAGTTTC 341

```

RESULT 12

```

CA220522
LOCUS SCRUF4023E04.g FL4 Saccharum officinarum cDNA clone SCRUF4023E04
DEFINITION 5', mRNA sequence.
ACCESSION CA220522
VERSION CA220522.1 GI:35273911
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
complex.
REFERENCE 1 (bases 1 to 669)
AUTHORS Vettore,A.L., da Silva,P.R., Kemper,E.L. and Arruda,P.
TITLE The libraries that made SUCEST
JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br

```

Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at <http://www.bcccenter.fcav.unesp.br>
 Plate: 023 row: E column: 04
 Seq primer: T7 Promoter Primer.

FEATURES

source

```

1..669
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCRUF4023E04"
/lab_host="DH10B"
/clone_lib="FL4"

```

/note="Organ: Developed inflorescence and rachis (20cm-long); Vector: pSport1; Site 1: SalI; Site 2: NotI; An unidirectional cDNA library generated from [Developed inflorescence and rachis (20cm-long)]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing

ORIGIN

```

Query Match      4.9%; Score 147.8; DB 6; Length 669;
Best Local Similarity 86.2%; Pred. No. 1.1e-28;
Matches 175; Conservative 0; Mismatches 27; Indels 1; Gaps 1;

QY 1458 TAAGCCAGTCTCAGTGGGGTTTCATCAGAGTTTCATGGAATTAAATAAGCTGATGTA 1517
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 427 TAAGCCAGTCTCAAT-GAGTTTCATCAGAGTTTCATAGACATTAAATATGCTGATGG 485

QY 1518 CACCGTATTGATGAAGAGAGAGATGATAAGAGTTTCATGCCAGTAGAGAGATTTCATGG 1577
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 486 TACATATTAAATGAAGAGAGATGATAAGAGTTTCATGGAGTAGAGAGATTTCATGG 545

QY 1578 GGATGAACCTCTTCTTCACTGTTTCCAAAATATAGATGCATTTGGTAAAGAGGCCATGAAA 1637
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 546 GGATGAACCTCTTCTGCACTGTTTCCAAAATCTGATGTGTTGGAAACAGTGACATGAAA 605

QY 1638 TCTCTAGTGCACCTGACCTAAGA 1660
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 606 TTCCCACTGAGACTGGCCTAATA 628

```

RESULT 13

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CL191874
LOCUS CL191874.1 GI:40704397
DEFINITION 740 bp DNA linear GSS 06-JAN-2004
104 414 10939851 114 32247 012 Sorghum methylation-filtered library
(LibID: 104) Sorghum bicolor genomic clone 10939851, genomic survey
sequence.
ACCESSION CL191874
VERSION CL191874.1
KEYWORDS GSS.
SOURCE Sorghum bicolor (sorghum)
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE 1 (bases 1 to 740)
AUTHORS Budiman,M.A., Flick,E., Jones,J., Nunberg,A., Citek,R.W.,
Robbins,D., Rohlfing,T., Bradford,K., Fries,J., McMenamy,J.,
Trani,L., Ieak,A., Zimmerman,C., Lakey,N. and Bedell,J.A.
TITLE GeneThresher methylation filtered genomic sequences from Sorghum
bicolor
JOURNAL Unpublished (2004)
COMMENT Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 414 row: f column: 03
Seq primer: M13/pUC Forward
Class: shotgun
High quality sequence stop: 740.

```

FEATURES

source

```

1..740
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="ATx623"
/db_xref="taxon:4558"
/clone="10939851"
/clone_lib="Sorghum methylation-filtered library (LibID: 104)"

```

/note="Organ: leaf; Vector: pBCSK(-); Site 1: HincII; DNA prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBCSK(-) vector and electroporated into *E. coli* cells. This is a methylation-filtered library."

between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at <http://sucst.lad.ic.unicamp.br/public>

ORIGIN

Query Match 4.9%; Score 147.4; DB 9; Length 740;
 Best Local Similarity 74.2%; Pred. No. 1.4e-28;
 Matches 241; Conservative 0; Mismatches 76; Indels 8; Gaps 4;

QY 1340 ACATTAGTTGGTATCATTAATATTATAT--TATCATATAAATTTGATCAACTTGAG 1397
 |||||
 Db 220 ACCTTAGTTGATATCATATAAATATTATATCTACCATATATTTGGTTAAACTTAAG 279
 |||||

QY 1398 ATGCTTTGACTCTTCAAGATTTCTTGAATCACTTATCATTTGGGGTAGGGAGTAGGTTTC 1457
 |||||
 Db 280 ATGCTTTAACTATCTAAGATTTTGGAAATGACTTGTCAITTTGGACGGAGGAGTAATCC 339
 |||||

QY 1458 TAAGGCCAGTCTCAGTGGGGTTTCATCAGAGTTTCATGACATTAATAAGCTGATGTA 1517
 |||||
 Db 340 TTAGGCCAGTCTCAATGGGATTTTCATAGAGTTTCATGCACATTAATATGC--ATATGA 397
 |||||

QY 1518 CACGCTATTGATGAAGAGAGAGATGATAAGAGTTTCATCGAGTACAGAGAGTTTCATGG 1577
 |||||
 Db 398 CATGTATTTATGA--AGAGAGATGATAGAAATTCATAAAGTAGAAATATTTTATCC 455
 |||||

QY 1578 GGATGAACACTCTTCTTCACTGTTTCCAAA--TATAGATGCATTTGTTAGAGGGCCATGA 1635
 |||||
 Db 456 CTATAAACTCTTTTGGCTATTTTAAATCTAAATATGTTAGAACTAGATCATCA 515
 |||||

QY 1636 AATCTCTAGTACACTGACCTAAGA 1660
 |||||
 Db 516 AATTACGATTGATGGGCTTAA 540
 |||||

RESULT 14

BZ693362
 LOCUS 1273 bp DNA linear GSS 02-JUL-2003
 DEFINITION SP_Ba0033E12.rp_Ba Sorghum propinquum genomic clone
 SP_Ba0033E12 3', Genomic survey sequence.

ACCESSION BZ693362
 VERSION BZ693362.1 GI:28385166
 KEYWORDS GSS.
 SOURCE Sorghum propinquum
 ORGANISM Sorghum propinquum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Sorghum.
 1 (bases 1 to 1273)
 Rabinowicz,P.D., O'Shaughnessy,A.L., Balijs,V., Dedhia,N.,
 Katzenburger,F., King,L., Miller,B., Muller,S., Nascimbeno,L.,
 Zutavern,T., Palmer,L., McCombie,W.R. and Martienssen,R.A.
 Genomic shotgun sequences from Sorghum bicolor (methyl-filtered)
 Unpublished (2002)
 Contact: W. Richard McCombie
 Lita Amentberg Hazen Genome Sequencing Center
 PO Box 100, Cold Spring Harbor, NY 11724, USA
 Tel: 516 367 8884
 Fax: 516 367 8874
 Email: mcombie@cshl.org
 Plate: ic83 row: e column: 09
 Seq primer: -21M13UnivRev
 Class: shotgun
 High quality sequence stop: 787.

JOURNAL

COMMENT

Arizona Genomics Institute
 University of Arizona
 Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
 85721-0088, USA
 Tel: 520 626 3967
 Fax: 520 621 9288
 Email: http://genome.arizona.edu
 PCR Primers
 FORWARD: atc agc ggc cgc gat cc
 BACKWARD: gta aaa cga cgg cca gtc
 Plate: 0033 row: E column: 12
 Seq primer: gta aaa cga cgg cca gtc
 Class: BAC ends.

FEATURES

source

1. .1273
 /organism="Sorghum propinquum"
 /mol_type="genomic DNA"
 /db_xref="taxon:132711"
 /clone="SP_Ba0033E12"
 /clone_lib="SP_Ba"
 /note="Vector: pBelobAC11; Site_1: HindIII; Site_2:
 HindIII; Paterson lab BAC library (HindIII)"

ORIGIN

Query Match 4.7%; Score 141.8; DB 8; Length 1273;
 Best Local Similarity 82.2%; Pred. No. 5.8e-27;
 Matches 175; Conservative 0; Mismatches 37; Indels 1; Gaps 1;

QY 1455 TTCTAAGCCAGTCTCAGTGGGTTTCATCAGAGTTTCATGACATTAATAAGCTGATG 1514
 |||||
 Db 130 TACTAAGGCCAGTCTCAAT--GGGTTTTCATTAGAGTTTCATGATATTAATATGCTGATG 188
 |||||

QY 1515 TGACACCGTATTGATGAAGAGAGAGATGATAAGAGTTTCATCGAGTAGAGAGAGTTTCA 1574
 |||||
 Db 189 TGGCACCGTATTAAATGAATAATAGAGGTGATAGAGTTTCATGAGAGTAGTAGAGATTTA 248
 |||||

QY 1575 TGGGGATGAAACTCTTCTTCACTGTTTCCAAAATATAGATGCATTTGGTAAGGGGCCCATG 1634
 |||||
 Db 249 TAGGGATGAACTCTTGTACATTTGTTTAAATATGATGTTTGGAACTAGACCCATG 308
 |||||

QY 1635 AATCTCTAGTACACTGACCTACCTAAGATGATTT 1667
 |||||
 Db 309 AAACCTACACTGAGAATGATCTAAGAGTCTATT 341
 |||||

RESULT 15

BZ342445
 LOCUS 787 bp DNA linear GSS 06-NOV-2002
 DEFINITION ic83e09.g1 WGS-SbicolorF (JM107 adapted methyl filtered) Sorghum
 bicolor genomic clone ic83e09 5', genomic survey sequence.

ACCESSION BZ342445

VERSION BZ342445.1 GI:24743123

KEYWORDS GSS.

SOURCE Sorghum bicolor (sorghum)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Sorghum.
 1 (bases 1 to 787)

REFERENCE

AUTHORS

Rabinowicz,P.D., O'Shaughnessy,A.L., Balijs,V., Dedhia,N.,
 Katzenburger,F., King,L., Miller,B., Muller,S., Nascimbeno,L.,
 Zutavern,T., Palmer,L., McCombie,W.R. and Martienssen,R.A.
 Genomic shotgun sequences from Sorghum bicolor (methyl-filtered)
 Unpublished (2002)

TITLE

JOURNAL

COMMENT

Contact: W. Richard McCombie
 Lita Amentberg Hazen Genome Sequencing Center
 PO Box 100, Cold Spring Harbor, NY 11724, USA
 Tel: 516 367 8884
 Fax: 516 367 8874
 Email: mcombie@cshl.org
 Plate: ic83 row: e column: 09
 Seq primer: -21M13UnivRev
 Class: shotgun
 High quality sequence stop: 787.

FEATURES

source

1. .787
 /organism="Sorghum bicolor"
 /mol_type="genomic DNA"
 /db_xref="taxon:4558"
 /clone="ic83e09"
 /lab_host="JM107 or DH5a"
 /clone_lib="WGS-SbicolorF (JM107 adapted methyl filtered)"
 /note="Site 1: Xba I; Site 2: Xba I; The vector was fill in
 digested with XbaI and one nucleotide was added by fill in
 in the recessive 3' end. The genomic DNA was nebulized,
 end repaired, adaptor ligated and size fractionated using
 sephadex. The resulting fragments were between 0.8 and 3
 kb and were cloned into the vector (x/y reads in M13mp19,
 b/g reads in pUC19). The same ligation was transformed in
 either JM107 or DH5a."

ORIGIN

Query Match 4.6%; Score 139.4; DB 8; Length 787;
 Best Local Similarity 82.3%; Pred. No. 2.3e-26;

	Matches 172;	Conservative 0;	Mismatches 36;	Indels 1;	Gaps 1;
Qy 1458	TAAGGCCAGTCTCAGTGGG-GTTTCATCAGAGTTCATGGACATTAATAAGCTCATGTG				1516
Db					
Qy 186	TTAGGCCAGTCTCAATGGGTGTTTCATTAGAGTTTCATGCACATTAATAATGCTGATGTG				245
Db					
Qy 1517	ACACCGTATTGATGAAGAGAGAGATGATAAGAGTTCATGCCAGTAGAGAGAGTTTCATG				1576
Db					
Qy 246	GCACATATTAAATGACAAGAGAGATGATAAGAGTTCATGGAGTAGAGAGAGTTTCATC				305
Db					
Qy 1577	GGGATGAACCTCTTCTTCACTGTTTCCAAAATATAGATGCATTTGGTAAGAGGGCCATGAA				1636
Db					
Qy 306	CCCATGAAATTCCTGTGCACCTGTTCCAAAATATTGATGATTGGAAACTGGGTCAATGAA				365
Db					
Qy 1637	ATCTCTAGTGACACTGACCTAAGATGAGA				1665
Db					
Qy 366	ACCTCCATTGAGGATGGCCTTAGAACACA				394
Db					

Search completed: February 16, 2005, 10:23:23
 Job time : 9459 secs

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